



SEQUENCE LISTING

(1) GENERAL INFORMATION

- TO610
- (i) APPLICANT: BOIME, Irving  
MOYLE, William R.
  - (ii) TITLE OF THE INVENTION: SINGLE-CHAIN FORMS OF THE  
GLYCOPROTEIN HORMONE QUARTET
  - (iii) NUMBER OF SEQUENCES: 83
  - (iv) CORRESPONDENCE ADDRESS:
    - (A) ADDRESSEE: MORRISON & FOERSTER
    - (B) STREET: 2000 Pennsylvania Avenue, NW, suite 5500
    - (C) CITY: Washington
    - (D) STATE: DC
    - (E) COUNTRY: USA
    - (F) ZIP: 20006-1888
  - (v) COMPUTER READABLE FORM:
    - (A) MEDIUM TYPE: Diskette
    - (B) COMPUTER: IBM Compatible
    - (C) OPERATING SYSTEM: DOS
    - (D) SOFTWARE: FastSEQ for Windows Version 2.0
  - (vi) CURRENT APPLICATION DATA:
    - (A) APPLICATION NUMBER: 08/918,288
    - (B) FILING DATE: 25 AUG-1997
    - (C) CLASSIFICATION:
  - (vii) PRIOR APPLICATION DATA:
    - (A) APPLICATION NUMBER: 08/853,524
    - (B) FILING DATE: 09-MAY-1997
    - (A) APPLICATION NUMBER: 08/199,382
    - (B) FILING DATE: 18-FEB-1994
  - (viii) ATTORNEY/AGENT INFORMATION:
    - (A) NAME: Murashige, Kate H
    - (B) REGISTRATION NUMBER: 29,959
    - (C) REFERENCE/DOCKET NUMBER: 29500-20050.25
  - (ix) TELECOMMUNICATION INFORMATION:
    - (A) TELEPHONE: 202-887-1500
    - (B) TELEFAX: 202-887-0763
    - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 amino acids
  - (B) TYPE: amino acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ser	Ser	Ser	Ser	Lys	Ala	Pro	Pro	Pro	Ser	Leu	Pro	Ser	Pro	Ser	Arg
1				5					10					15	
Leu	Pro	Gly	Pro	Ser	Asp	Thr	Pro	Ile	Leu	Pro	Gln				
			20					25							

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 836 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
(B) LOCATION: 33...827  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGAAATCGA	CGGAATCAGA	CTCGAGCCAA	GG	ATG	GAG	ATG	TTC	CAG	GGG	CTG	53
			1	Met	Glu	Met	Phe	Gln	Gly	Leu	
CTG	CTG	TTG	CTG	CTG	CTG	AGC	ATG	GGC	GGG	ACA	101
Leu	Leu	Leu	Leu	Leu	Leu	Ser	Met	Gly	Gly	Thr	
		10				15				20	
CCG	CTT	CGG	CCA	CGG	TGC	CGC	CCC	ATC	AAT	GCC	149
Pro	Leu	Arg	Pro	Arg	Cys	Arg	Pro	Ile	Asn	Ala	
	25				30				35		
AAG	GAG	GGC	TGC	CCC	GTG	TGC	ATC	ACC	GTC	AAC	197
Lys	Glu	Gly	Cys	Pro	Val	Cys	Ile	Thr	Val	Asn	
40			45						50		
GGC	TAC	TGC	CCC	ACC	ATG	ACC	CGC	GTG	CTG	CAG	245
Gly	Tyr	Cys	Pro	Thr	Met	Thr	Arg	Val	Leu	Gln	
			60					65		70	
CTG	CCT	CAG	GTG	GTG	TGC	AAC	TAC	CGC	GAT	GTG	293
Leu	Pro	Gln	Val	Val	Cys	Asn	Tyr	Arg	Asp	Val	
		75				80				85	
CGG	CTC	CCT	GGC	TGC	CCG	CGC	GGC	GTG	AAC	CCC	341
Arg	Leu	Pro	Gly	Cys	Pro	Arg	Gly	Val	Asn	Pro	
		90				95				100	
GTG	GCT	CTC	AGC	TGT	CAA	TGT	GCA	CTC	TGC	CGC	389
Val	Ala	Leu	Ser	Cys	Gln	Cys	Ala	Leu	Cys	Arg	

62

105	110	115	
TGC GGG GGT CCC AAG GAC CAC CCC TTG ACC TGT GAT GAC CCC CGC TTC			437
Cys Gly Gly Pro Lys Asp His Pro Leu Thr Cys Asp Asp Pro Arg Phe			
120	125	130	135
CAG GAC TCC TCT TCC TCA AAG GCC CCT CCC CCC AGC CTT CCA AGC CCA			485
Gln Asp Ser Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu Pro Ser Pro			
	140	145	150
TCC CGA CTC CCG GGG CCC TCG GAC ACC CCG ATC CTC CCC CAA GGA TCC			533
Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro Gln Gly Ser			
	155	160	165
GGT AGC GGA TCT GGT AGC GCT CCT GAT GTG CAG GAT TGC CCA GAA TGC			581
Gly Ser Gly Ser Gly Ser Ala Pro Asp Val Gln Asp Cys Pro Glu Cys			
	170	175	180
ACG CTA CAG GAA AAC CCA TTC TTC TCC CAG CCG GGT GCC CCA ATA CTT			629
Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile Leu			
	185	190	195
CAG TGC ATG GGC TGC TGC TTC TCT AGA GCA TAT CCC ACT CCA CTA AGG			677
Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro Leu Arg			
200	205	210	215
TCC AAG AAG ACG ATG TTG GTC CAA AAG AAC GTC ACC TCA GAG TCC ACT			725
Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser Glu Ser Thr			
	220	225	230
TGC TGT GTA GCT AAA TCA TAT AAC AGG GTC ACA GTA ATG GGG GGT TTC			773
Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met Gly Gly Phe			
	235	240	245
AAA GTG GAG AAC CAC ACG GCG TGC CAC TGC AGT ACT TGT TAT TAT CAC			821
Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr Tyr His			
	250	255	260
AAA TCT TAAGGTACC			836
Lys Ser			
265			

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Glu Met Phe Gln Gly Leu Leu Leu Leu Leu Leu Ser Met Gly

1	5	10	15
Gly Thr Trp Ala Ser Lys Glu Pro Leu Arg Pro Arg Cys Arg Pro Ile			
	20	25	30
Asn Ala Thr Leu Ala Val Glu Lys Glu Gly Cys Pro Val Cys Ile Thr			
	35	40	45
Val Asn Thr Thr Ile Cys Ala Gly Tyr Cys Pro Thr Met Thr Arg Val			
	50	55	60
Leu Gln Gly Val Leu Pro Ala Leu Pro Gln Val Val Cys Asn Tyr Arg			
	65	70	75
Asp Val Arg Phe Glu Ser Ile Arg Leu Pro Gly Cys Pro Arg Gly Val			
	85	90	95
Asn Pro Val Val Ser Tyr Ala Val Ala Leu Ser Cys Gln Cys Ala Leu			
	100	105	110
Cys Arg Arg Ser Thr Thr Asp Cys Gly Gly Pro Lys Asp His Pro Leu			
	115	120	125
Thr Cys Asp Asp Pro Arg Phe Gln Asp Ser Ser Ser Ser Lys Ala Pro			
	130	135	140
Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr			
	145	150	155
Pro Ile Leu Pro Gln Gly Ser Gly Ser Gly Ser Gly Ser Ala Pro Asp			
	165	170	175
Val Gln Asp Cys Pro Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser			
	180	185	190
Gln Pro Gly Ala Pro Ile Leu Gln Cys Met Gly Cys Cys Phe Ser Arg			
	195	200	205
Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys			
	210	215	220
Asn Val Thr Ser Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg			
	225	230	235
Val Thr Val Met Gly Phe Lys Val Glu Asn His Thr Ala Cys His			
	245	250	255
Cys Ser Thr Cys Tyr Tyr His Lys Ser			
	260	265	

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TCCGGATTAG	CTTGAGATGG	ATCCGGTACC	TTAAGATTTG	TGATAATAAC	AAGTACTGCA	60
GTGGCACGCC	GTGTGGTTCT	CCACTTTGAA	ACCCCCATT	ACTGTGACCC	TGTTATATGA	120
TTTAGCTACA	CAGCAAGTGG	ACTCTGAGGT	GACGTTCTTT	TGGACCAACA	TCGCTTCTTT	180
GGACCTTAGT	GGAGTGGGAT	ATGCTCTAGA	GAAGCAGCAG	CCCATGCACT	GAAGTATTGG	240
GGCACCCGGC	TGGGAGAAGA	ATGGGTTTTT	CTGTAGCGTG	CATTCTGGGC	AATCCTGCAC	300
ATCAGGAGCG	CTACCAGATC	CGCTACCGGA	TCCTTGGGGG	AGGATCGGGG	TGTCCGAGGG	360
CCCCGGGAGT	CGGGATGGGC	TTGGAAGGCT	GGGGGGAGGG	GCCTTTGAGG	AAGAGGAGTC	420
CTGGAAGCGG	GGGTCATCAC	AGGTCAAGGG	GTGGTCCTTG	GGACCCCCGC	AGTCAGTGGT	480
GCTGCGGCGG	CAGAGTGCAC	ATTGACAGCT	GAGAGCCACG	GCGTAGGAGA	CCACGGGGTT	540
CACGCCGCGC	GGGCAGCCAG	GGAGCCGGAT	GGACTCGAAG	CGCACATCGC	GGTAGTTGCA	600
CACCACCTGA	GGCAGGGCCG	GCAGGACCCC	CTGCAGCACG	CGGGTCATGG	TGGGGCAGTA	660
GCCGGCACAG	ATGGTGGTGT	TGACGGTGAT	GCACACGGGG	CAGCCCTCCT	TCTCCACAGC	720

64

CAGGGTGGCA TTGATGGGGC GGCACCGTGG CCGAAGCGGC TCCTTGGATG CCCATGTCCC 780  
 GCCCATGCTC AGCAGCAGCA ACAGCAGCAG CCCCTGGAAC ATCTCCATCC TTGG 834

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 743 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 33...734
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGAAATCGA CGGAATCAGA CTCGAGCCAA GG	ATG GAG ATG TTC CAG GGG CTG	53
	Met Glu Met Phe Gln Gly Leu	
	1 5	
CTG CTG TTG CTG CTG CTG AGC ATG GGC GGG ACA TGG GCA TCC AAG GAG	101	
Leu Leu Leu Leu Leu Leu Ser Met Gly Gly Thr Trp Ala Ser Lys Glu		
10 15 20		
CCG CTT CGG CCA CGG TGC CGC CCC ATC AAT GCC ACC CTG GCT GTG GAG	149	
Pro Leu Arg Pro Arg Cys Arg Pro Ile Asn Ala Thr Leu Ala Val Glu		
25 30 35		
AAG GAG GGC TGC CCC GTG TGC ATC ACC GTC AAC ACC ACC ATC TGT GCC	197	
Lys Glu Gly Cys Pro Val Cys Ile Thr Val Asn Thr Thr Ile Cys Ala		
40 45 50 55		
GGC TAC TGC CCC ACC ATG ACC CGC GTG CTG CAG GGG GTC CTG CCG GCC	245	
Gly Tyr Cys Pro Thr Met Thr Arg Val Leu Gln Gly Val Leu Pro Ala		
60 65 70		
CTG CCT CAG GTG GTG TGC AAC TAC CGC GAT GTG CGC TTC GAG TCC ATC	293	
Leu Pro Gln Val Val Cys Asn Tyr Arg Asp Val Arg Phe Glu Ser Ile		
75 80 85		
CGG CTC CCT GGC TGC CCG CGC GGC GTG AAC CCC GTG GTC TCC TAC GCC	341	
Arg Leu Pro Gly Cys Pro Arg Gly Val Asn Pro Val Val Ser Tyr Ala		
90 95 100		
GTG GCT CTC AGC TGT CAA TGT GCA CTC TGC CGC CGC AGC ACC ACT GAC	389	
Val Ala Leu Ser Cys Gln Cys Ala Leu Cys Arg Ser Thr Thr Asp		
105 110 115		
TGC GGG GGT CCC AAG GAC CAC CCC TTG ACC TGT GAT GAC CCG CGG GGA	437	
Cys Gly Gly Pro Lys Asp His Pro Leu Thr Cys Asp Asp Pro Arg Gly		
120 125 130 135		
TCC GGT AGC GGA TCT GGT AGC GCT CCT GAT GTG CAG GAT TGC CCA GAA	485	
Ser Gly Ser Gly Ser Gly Ser Ala Pro Asp Val Gln Asp Cys Pro Glu		

130		135		140
Asp Val Gln Asp Cys Pro Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe				
145		150		155
Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys Met Gly Cys Cys Phe Ser				160
	165		170	175
Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln				
	180		185	190
Lys Asn Val Thr Ser Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn				
	195		200	205
Arg Val Thr Val Met Gly Gly Phe Lys Val Glu Asn His Thr Ala Cys				
	210		215	220
His Cys Ser Thr Cys Tyr Tyr His Lys Ser				
225		230		

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 717 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGTACCTTAA GATTTGTGAT AATAACAAGT ACTGCAGTGG CACGCCGTGT GGTTCTCCAC	60
TTTGAAACCC CCCATTACTG TGACCCTGTT ATATGATTTA GCTACACAGC AAGTGGACTC	120
TGAGGTGACG TTCTTTTGGG CCAACATCGT CTTCTTGGAC CTTAGTGGAG TGGGATATGC	180
TCTAGAGAAG CAGCAGCCCA TGCCTGAAG TATTGGGGCA CCCGGCTGGG AGAAGAATGG	240
GTTTTCTGT AGCGTGCAAT CTGGGCAATC CTGCACATCA GGAGCGCTAC CAGATCCGCT	300
ACCGGATCCC CGCGGGTCAT CACAGGTCAA GGGGTGGTCC TTGGGACCCC CGCAGTCAGT	360
GGTGCTGCGG CGGCAGAGTG CACATTGACA GCTGAGAGCC ACGGCGTAGG AGACCACGGG	420
GTTACGCGCG CGCGGGCAGC CAGGGAGCCG GATGGACTCG AAGCGCACAT CGCGGTAGTT	480
GCACACCACC TGAGGCAGGG CCGGCAGGAC CCCCTGCAGC ACGCGGGTCA TGGTGGGGCA	540
GTAGCCGGCA CAGATGGTGG TGTGACGGT GATGCACACG GGGCAGCCCT CCTTCTCCAC	600
AGCCAGGGTG GCATTGATGG GCGGCACCG TGGCCGAAGC GGCTCCTTGG ATGCCCATGT	660
CCCGCCCATG CTCAGCAGCA GCAACAGCAG CAGCCCCTGG AACATCTCCA TCCTTGG	717

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 744 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 34...735
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGAAATCGA CGGAATCAGA CTCGAGCCAA GGA ATG GAG ATG CTC CAG GGG CTG	54
Met Glu Met Leu Gln Gly Leu	
1 5	

140										145					150					
TGC	ACG	CTA	CAG	GAA	AAC	CCA	TTC	TTC	TCC	CAG	CCG	GGT	GCC	CCA	ATA	533				
Cys	Thr	Leu	Gln	Glu	Asn	Pro	Phe	Phe	Ser	Gln	Pro	Gly	Ala	Pro	Ile					
			155						160			165								
CTT	CAG	TGC	ATG	GGC	TGC	TGC	TTC	TCT	AGA	GCA	TAT	CCC	ACT	CCA	CTA	581				
Leu	Gln	Cys	Met	Gly	Cys	Cys	Phe	Ser	Arg	Ala	Tyr	Pro	Thr	Pro	Leu					
			170						175			180								
AGG	TCC	AAG	AAG	ACG	ATG	TTG	GTC	CAA	AAG	AAC	GTC	ACC	TCA	GAG	TCC	629				
Arg	Ser	Lys	Lys	Thr	Met	Leu	Val	Gln	Lys	Asn	Val	Thr	Ser	Glu	Ser					
			185						190			195								
ACT	TGC	TGT	GTA	GCT	AAA	TCA	TAT	AAC	AGG	GTC	ACA	GTA	ATG	GGG	GGT	677				
Thr	Cys	Cys	Val	Ala	Lys	Ser	Tyr	Asn	Arg	Val	Thr	Val	Met	Gly	Gly					
200						205						210			215					
TTC	AAA	GTG	GAG	AAC	CAC	ACG	GCG	TGC	CAC	TGC	AGT	ACT	TGT	TAT	TAT	725				
Phe	Lys	Val	Glu	Asn	His	Thr	Ala	Cys	His	Cys	Ser	Thr	Cys	Tyr	Tyr					
			220						225			230								
CAC AAA TCT TAAGGTACC															743					
His Lys Ser																				

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Glu	Met	Phe	Gln	Gly	Leu	Leu	Leu	Leu	Leu	Leu	Ser	Met	Gly
1				5				10					15	
Gly	Thr	Trp	Ala	Ser	Lys	Glu	Pro	Leu	Arg	Pro	Arg	Cys	Arg	Pro
			20					25				30		Ile
Asn	Ala	Thr	Leu	Ala	Val	Glu	Lys	Glu	Gly	Cys	Pro	Val	Cys	Ile
			35					40				45		Thr
Val	Asn	Thr	Thr	Ile	Cys	Ala	Gly	Tyr	Cys	Pro	Thr	Met	Thr	Arg
			50					55				60		Val
Leu	Gln	Gly	Val	Leu	Pro	Ala	Leu	Pro	Gln	Val	Val	Cys	Asn	Tyr
														80
Asp	Val	Arg	Phe	Glu	Ser	Ile	Arg	Leu	Pro	Gly	Cys	Pro	Arg	Gly
				85										95
Asn	Pro	Val	Val	Ser	Tyr	Ala	Val	Ala	Leu	Ser	Cys	Gln	Cys	Ala
			100					105					110	Leu
Cys	Arg	Arg	Ser	Thr	Thr	Asp	Cys	Gly	Gly	Pro	Lys	Asp	His	Pro
			115					120				125		Leu
Thr	Cys	Asp	Asp	Pro	Arg	Gly	Ser	Gly	Ser	Gly	Ser	Gly	Ser	Ala
														Pro

CTG CTG TTG CTG CTG CTG AGC ATG GGC GGG GCA TGG GCA TCC AGG GAG	102
Leu Leu Leu Leu Leu Leu Ser Met Gly Gly Ala Trp Ala Ser Arg Glu	
10 15 20	
CCG CTT CGG CCA TGG TGC CAC CCC ATC AAT GCC ATC CTG GCT GTG GAG	150
Pro Leu Arg Pro Trp Cys His Pro Ile Asn Ala Ile Leu Ala Val Glu	
25 30 35	
AAG GAG GGC TGC CCC GTG TGC ATC ACC GTC AAC ACC ACC ATC TGT GCC	198
Lys Glu Gly Cys Pro Val Cys Ile Thr Val Asn Thr Thr Ile Cys Ala	
40 45 50 55	
GGC TAC TGC CCC ACC ATG ATG CGC GTG CTG CAG GCG GTC CTG CCG CCC	246
Gly Tyr Cys Pro Thr Met Met Arg Val Leu Gln Ala Val Leu Pro Pro	
60 65 70	
CTG CCT CAG GTG GTG TGC ACC TAC CGT GAT GTG CGC TTC GAG TCC ATC	294
Leu Pro Gln Val Val Cys Thr Tyr Arg Asp Val Arg Phe Glu Ser Ile	
75 80 85	
CGG CTC CCT GGC TGC CCG CGT GGC GTG GAC CCC GTG GTC TCC TTC CCT	342
Arg Leu Pro Gly Cys Pro Arg Gly Val Asp Pro Val Val Ser Phe Pro	
90 95 100	
GTG GCT CTC AGC TGT CGC TGT GGA CCC TGC CGC CGC AGC ACC TCT GAC	390
Val Ala Leu Ser Cys Arg Cys Gly Pro Cys Arg Arg Ser Thr Ser Asp	
105 110 115	
TGT GGG GGT CCC AAA GAC CAC CCC TTG ACC TGT GAC CAC CCC CAA GGA	438
Cys Gly Gly Pro Lys Asp His Pro Leu Thr Cys Asp His Pro Gln Gly	
120 125 130 135	
TCC GGT AGC GGA TCT GGT AGC GCT CCT GAT GTG CAG GAT TGC CCA GAA	486
Ser Gly Ser Gly Ser Gly Ser Ala Pro Asp Val Gln Asp Cys Pro Glu	
140 145 150	
TGC ACG CTA CAG GAA AAC CCA TTC TTC TCC CAG CCG GGT GCC CCA ATA	534
Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile	
155 160 165	
CTT CAG TGC ATG GGC TGC TGC TTC TCT AGA GCA TAT CCC ACT CCA CTA	582
Leu Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro Leu	
170 175 180	
AGG TCC AAG AAG ACG ATG TTG GTC CAA AAG AAC GTC ACC TCA GAG TCC	630
Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser Glu Ser	
185 190 195	
ACT TGC TGT GTA GCT AAA TCA TAT AAC AGG GTC ACA GTA ATG GGG GGT	678
Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met Gly Gly	
200 205 210 215	
TTC AAA GTG GAG AAC CAC ACG GCG TGC CAC TGC AGT ACT TGT TAT TAT	726
Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr Tyr	
220 225 230	

68



CAC AAA TCT TAAGGTACC  
His Lys Ser

744

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met	Glu	Met	Leu	Gln	Gly	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Ser	Met	Gly
1				5				10						15	
Gly	Ala	Trp	Ala	Ser	Arg	Glu	Pro	Leu	Arg	Pro	Trp	Cys	His	Pro	Ile
			20					25					30		
Asn	Ala	Ile	Leu	Ala	Val	Glu	Lys	Glu	Gly	Cys	Pro	Val	Cys	Ile	Thr
		35					40					45			
Val	Asn	Thr	Thr	Ile	Cys	Ala	Gly	Tyr	Cys	Pro	Thr	Met	Met	Arg	Val
	50					55					60				
Leu	Gln	Ala	Val	Leu	Pro	Leu	Pro	Gln	Val	Val	Cys	Thr	Tyr	Arg	
65					70				75					80	
Asp	Val	Arg	Phe	Glu	Ser	Ile	Arg	Leu	Pro	Gly	Cys	Pro	Arg	Gly	Val
				85					90					95	
Asp	Pro	Val	Val	Ser	Phe	Pro	Val	Ala	Leu	Ser	Cys	Arg	Cys	Gly	Pro
			100					105					110		
Cys	Arg	Arg	Ser	Thr	Ser	Asp	Cys	Gly	Gly	Pro	Lys	Asp	His	Pro	Leu
		115					120					125			
Thr	Cys	Asp	His	Pro	Gln	Gly	Ser	Gly	Ser	Gly	Ser	Gly	Ser	Ala	Pro
	130					135					140				
Asp	Val	Gln	Asp	Cys	Pro	Glu	Cys	Thr	Leu	Gln	Glu	Asn	Pro	Phe	Phe
145					150					155				160	
Ser	Gln	Pro	Gly	Ala	Pro	Ile	Leu	Gln	Cys	Met	Gly	Cys	Cys	Phe	Ser
				165					170					175	
Arg	Ala	Tyr	Pro	Thr	Pro	Leu	Arg	Ser	Lys	Lys	Thr	Met	Leu	Val	Gln
			180					185					190		
Lys	Asn	Val	Thr	Ser	Glu	Ser	Thr	Cys	Cys	Val	Ala	Lys	Ser	Tyr	Asn
	195						200					205			
Arg	Val	Thr	Val	Met	Gly	Gly	Phe	Lys	Val	Glu	Asn	His	Thr	Ala	Cys
	210					215					220				
His	Cys	Ser	Thr	Cys	Tyr	His	Lys	Ser							
225					230										

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 718 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGTACCTTAA GATTTGTGAT AATAACAAGT ACTGCAGTGG CACGCCGTGT GGTTCTCCAC	60
TTTGAAACCC CCCATTACTG TGACCCTGTT ATATGATTTA GCTACACAGC AAGTGGACTC	120
TGAGGTGACG TTCTTTTGGG CCAACATCGT CTTCTTGGAC CTTAGTGGAG TGGGATATGC	180
TCTAGAGAAG CAGCAGCCCA TGCACTGAAG TATTGGGGCA CCCGGCTGGG AGAAGAATGG	240
GTTTTCTGT AGCGTGCATT CTGGGCAATC CTGCACATCA GGAGCGCTAC CAGATCCGCT	300
ACCGGATCCT TGGGGGTGGT CACAGGTCAA GGGGTGGTCT TTGGGACCCC CACAGTCAGA	360
GGTGCTGCGG CGGCAGGGTC CACAGCGACA GCTGAGAGCC ACAGGGAAGG AGACCACGGG	420
GTCCACGCCA CGCGGGCAGC CAGGGAGCCG GATGGACTCG AAGCGCACAT CACGGTAGGT	480
GCACACCACC TGAGGCAGGG GCGGCAGGAC CGCCTGCAGC ACGCGCATCA TGGTGGGGCA	540
GTAGCCGGCA CAGATGGTGG TGTTGACGGT GATGCACACG GGGCAGCCCT CCTTCTCCAC	600
AGCCAGGATG GCATTGATGG GGTGGCACCA TGGCCGAAGC GGCTCCCTGG ATGCCCATGC	660
CCCGCCCATG CTCAGCAGCA GCAACAGCAG CAGCCCCTGG AGCATCTCCA TTCCTTGG	718

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 728 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 33...719
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATGAAATCGA CGGAATCAGA CTCGAGCCAA GG ATG AAG ACA CTC CAG TTT TTC	53
Met Lys Thr Leu Gln Phe Phe	
1 5	
TTC CTT TTC TGT TGC TGG AAA GCA ATC TGC TGC AAT AGC TGT GAG CTG	101
Phe Leu Phe Cys Cys Trp Lys Ala Ile Cys Cys Asn Ser Cys Glu Leu	
10 15 20	
ACC AAC ATC ACC ATT GCA ATA GAG AAA GAA GAA TGT CGT TTC TGC ATA	149
Thr Asn Ile Thr Ile Ala Ile Glu Lys Glu Glu Cys Arg Phe Cys Ile	
25 30 35	
AGC ATC AAC ACC ACT TGG TGT GCT GGC TAC TGC TAC ACC AGG GAT CTG	197
Ser Ile Asn Thr Thr Trp Cys Ala Gly Tyr Cys Tyr Thr Arg Asp Leu	
40 45 50 55	
GTG TAT AAG GAC CCA GCC AGG CCC AAA ATC CAG AAA ACA TGT ACC TTC	245
Val Tyr Lys Asp Pro Ala Arg Pro Lys Ile Gln Lys Thr Cys Thr Phe	
60 65 70	
AAG GAA CTG GTA TAT GAA ACA GTG AGA GTG CCC GGC TGT GCT CAC CAT	293
Lys Glu Leu Val Tyr Glu Thr Val Arg Val Pro Gly Cys Ala His His	
75 80 85	
GCA GAT TCC TTG TAT ACA TAC CCA GTG GCC ACC CAG TGT CAC TGT GGC	341

Ala	Asp	Ser	Leu	Tyr	Thr	Tyr	Pro	Val	Ala	Thr	Gln	Cys	His	Cys	Gly		
		90					95					100					
AAG	TGT	GAC	AGC	GAC	AGC	ACT	GAT	TGT	ACT	GTG	CGA	GGC	CTG	GGG	CCC	389	
Lys	Cys	Asp	Ser	Asp	Ser	Thr	Asp	Cys	Thr	Val	Arg	Gly	Leu	Gly	Pro		
	105					110					115						
AGC	TAC	TGC	TCC	TTT	GGT	GAA	ATG	AAA	GAA	GGA	TCC	GGT	AGC	GGA	TCT	437	
Ser	Tyr	Cys	Ser	Phe	Gly	Glu	Met	Lys	Glu	Gly	Ser	Gly	Ser	Gly	Ser		
	120				125					130					135		
GGT	AGC	GCT	CCT	GAT	GTG	CAG	GAT	TGC	CCA	GAA	TGC	ACG	CTA	CAG	GAA	485	
Gly	Ser	Ala	Pro	Asp	Val	Gln	Asp	Cys	Pro	Glu	Cys	Thr	Leu	Gln	Glu		
			140						145					150			
AAC	CCA	TTC	TTC	TCC	CAG	CCG	GGT	GCC	CCA	ATA	CTT	CAG	TGC	ATG	GGC	533	
Asn	Pro	Phe	Phe	Ser	Gln	Pro	Gly	Ala	Pro	Ile	Leu	Gln	Cys	Met	Gly		
		155						160					165				
TGC	TGC	TTC	TCT	AGA	GCA	TAT	CCC	ACT	CCA	CTA	AGG	TCC	AAG	AAG	ACG	581	
Cys	Cys	Phe	Ser	Arg	Ala	Tyr	Pro	Thr	Pro	Leu	Arg	Ser	Lys	Lys	Thr		
		170					175					180					
ATG	TTG	GTC	CAA	AAG	AAC	GTC	ACC	TCA	GAG	TCC	ACT	TGC	TGT	GTA	GCT	629	
Met	Leu	Val	Gln	Lys	Asn	Val	Thr	Ser	Glu	Ser	Thr	Cys	Cys	Val	Ala		
	185					190					195						
AAA	TCA	TAT	AAC	AGG	GTC	ACA	GTA	ATG	GGG	GGT	TTC	AAA	GTG	GAG	AAC	677	
Lys	Ser	Tyr	Asn	Arg	Val	Thr	Val	Met	Gly	Gly	Phe	Lys	Val	Glu	Asn		
	200				205					210				215			
CAC	ACG	GCG	TGC	CAC	TGC	AGT	ACT	TGT	TAT	TAT	CAC	AAA	TCT	TAAGGTACC	728		
His	Thr	Ala	Cys	His	Cys	Ser	Thr	Cys	Tyr	Tyr	His	Lys	Ser				
			220						225								

728

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met	Lys	Thr	Leu	Gln	Phe	Phe	Phe	Leu	Phe	Cys	Cys	Trp	Lys	Ala	Ile		
1				5				10						15			
Cys	Cys	Asn	Ser	Cys	Glu	Leu	Thr	Asn	Ile	Thr	Ile	Ala	Ile	Glu	Lys		
		20					25					30					
Glu	Glu	Cys	Arg	Phe	Cys	Ile	Ser	Ile	Asn	Thr	Thr	Trp	Cys	Ala	Gly		
	35					40					45						
Tyr	Cys	Tyr	Thr	Arg	Asp	Leu	Val	Tyr	Lys	Asp	Pro	Ala	Arg	Pro	Lys		

71

50		55		60
Ile Gln Lys Thr Cys Thr Phe Lys Glu Leu Val Tyr Glu Thr Val Arg				
65		70		75
Val Pro Gly Cys Ala His His Ala Asp Ser Leu Tyr Thr Tyr Pro Val				80
	85		90	95
Ala Thr Gln Cys His Cys Gly Lys Cys Asp Ser Asp Ser Thr Asp Cys				
	100		105	110
Thr Val Arg Gly Leu Gly Pro Ser Tyr Cys Ser Phe Gly Glu Met Lys				
	115		120	125
Glu Gly Ser Gly Ser Gly Ser Gly Ser Ala Pro Asp Val Gln Asp Cys				
	130		135	140
Pro Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala				
	145		150	155
Pro Ile Leu Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr				
	165		170	175
Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser				
	180		185	190
Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met				
	195		200	205
Gly Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys				
	210		215	220
Tyr Tyr His Lys Ser				
225				

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 702 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGTACCTTAA GATTTGTGAT AATAACAAGT ACTGCAGTGG CACGCCGTGT GGTTCCTCCAC	60
TTTGAAACCC CCCATTACTG TGACCCTGTT ATATGATTTA GCTACACAGC AAGTGGACTC	120
TGAGGTGACG TTCTTTTGGG CCAACATCGT CTTCTTGGAC CTTAGTGGAG TGGGATATGC	180
TCTAGAGAAG CAGCAGCCCA TGCCTGAAG TATTGGGGCA CCCGGCTGGG AGAAGAATGG	240
GTTTTCTGT AGCGTGCATT CTGGGCAATC CTGCACATCA GGAGCGCTAC CAGATCCGCT	300
ACCGGATCCT TCTTTTCATT CACCAAAGGA GCAGTAGCTG GGCCCCAGGC CTCGCACAGT	360
ACAATCAGTG CTGTGCTGT CACACTTGCC ACAGTGACAC TGGGTGGCCA CTGGGTATGT	420
ATACAAGGAA TCTGCATGGT GAGCACAGCC GGGCACTCTC ACTGTTTCAT ATACCAGTTC	480
CTTGAAGGTA CATGTTTTCT GGATTTTGGG CCTGGCTGGG TCCTTATACA CCAGATCCCT	540
GGTGTAGCAG TAGCCAGCAC ACCAAGTGGT GTTGATGCTT ATGCAGAAAC GACATTCTTC	600
TTTCTCTATT GCAATGGTGA TGTGGTCAG CTCACAGCTA TTGCAGCAGA TTGCTTTCCA	660
GCAACAGAAA AGGAAGAAAA ACTGGAGTGT CTTATCCTT GG	702

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 752 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

72

(A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 33...743  
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATGAAATCGA CGGAATCAGA CTCGAGCCAA GG	ATG GAG ATG TTC CAG GGG CTG	53
	Met Glu Met Phe Gln Gly Leu	
	1 5	
CTG CTG TTG CTG CTG CTG AGC ATG GGC GGG ACA TGG GCA TCC AAG GAG		101
Leu Leu Leu Leu Leu Leu Ser Met Gly Gly Thr Trp Ala Ser Lys Glu		
	10 15 20	
CCG CTT CGG CCA CGG TGC CGC CCC ATC AAT GCC ACC CTG GCT GTG GAG		149
Pro Leu Arg Pro Arg Cys Arg Pro Ile Asn Ala Thr Leu Ala Val Glu		
	25 30 35	
AAG GAG GGC TGC CCC GTG TGC ATC ACC GTC AAC ACC ACC ATC TGT GCC		197
Lys Glu Gly Cys Pro Val Cys Ile Thr Val Asn Thr Thr Ile Cys Ala		
	40 45 50 55	
GGC TAC TGC CCC ACC ATG ACC CGC GTG CTG CAG GGG GTC CTG CCG GCC		245
Gly Tyr Cys Pro Thr Met Thr Arg Val Leu Gln Gly Val Leu Pro Ala		
	60 65 70	
CTG CCT CAG GTG GTG TGC AAC TAC CGC GAT GTG CGC TTC GAG TCC ATC		293
Leu Pro Gln Val Val Cys Asn Tyr Arg Asp Val Arg Phe Glu Ser Ile		
	75 80 85	
CGG CTC CCT GGC TGC CCG CGC GGC GTG AAC CCC GTG GTC TCC TAC GCC		341
Arg Leu Pro Gly Cys Pro Arg Gly Val Asn Pro Val Val Ser Tyr Ala		
	90 95 100	
GTG GCT CTC AGC TGT CAA TGT GCA CTC TGC GAC AGC GAC AGC ACT GAT		389
Val Ala Leu Ser Cys Gln Cys Ala Leu Cys Asp Ser Asp Ser Thr Asp		
	105 110 115	
TGT ACT GTG CGA GGC CTG GGG CCC AGC TAC TGC TCC TTT GGT GAA ATG		437
Cys Thr Val Arg Gly Leu Gly Pro Ser Tyr Cys Ser Phe Gly Glu Met		
	120 125 130 135	
AAA GAA GGA TCC GGT AGC GGA TCT GGT AGC GCT CCT GAT GTG CAG GAT		485
Lys Glu Gly Ser Gly Ser Gly Ser Gly Ser Ala Pro Asp Val Gln Asp		
	140 145 150	
TGC CCA GAA TGC ACG CTA CAG GAA AAC CCA TTC TTC TCC CAG CCG GGT		533
Cys Pro Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly		
	155 160 165	
GCC CCA ATA CTT CAG TGC ATG GGC TGC TGC TTC TCT AGA GCA TAT CCC		581
Ala Pro Ile Leu Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro		
	170 175 180	
ACT CCA CTA AGG TCC AAG AAG ACG ATG TTG GTC CAA AAG AAC GTC ACC		629
Thr Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val Thr		

73

185		190		195	
TCA GAG TCC ACT TGC TGT GTA GCT AAA TCA TAT AAC AGG GTC ACA GTA					677
Ser Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val					
200		205		210	215
ATG GGG GGT TTC AAA GTG GAG AAC CAC ACG GCG TGC CAC TGC AGT ACT					725
Met Gly Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr					
	220		225		230
TGT TAT TAT CAC AAA TCT TAAGGTACC					752
Cys Tyr Tyr His Lys Ser					
	235				

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met	Glu	Met	Phe	Gln	Gly	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Ser	Met	Gly
1				5					10					15	
Gly	Thr	Trp	Ala	Ser	Lys	Glu	Pro	Leu	Arg	Pro	Arg	Cys	Arg	Pro	Ile
			20					25					30		
Asn	Ala	Thr	Leu	Ala	Val	Glu	Lys	Glu	Gly	Cys	Pro	Val	Cys	Ile	Thr
		35					40					45			
Val	Asn	Thr	Thr	Ile	Cys	Ala	Gly	Tyr	Cys	Pro	Thr	Met	Thr	Arg	Val
	50					55					60				
Leu	Gln	Gly	Val	Leu	Pro	Ala	Leu	Pro	Gln	Val	Val	Cys	Asn	Tyr	Arg
65					70				75					80	
Asp	Val	Arg	Phe	Glu	Ser	Ile	Arg	Leu	Pro	Gly	Cys	Pro	Arg	Gly	Val
				85				90						95	
Asn	Pro	Val	Val	Ser	Tyr	Ala	Val	Ala	Leu	Ser	Cys	Gln	Cys	Ala	Leu
			100					105					110		
Cys	Asp	Ser	Asp	Ser	Thr	Asp	Cys	Thr	Val	Arg	Gly	Leu	Gly	Pro	Ser
	115					120						125			
Tyr	Cys	Ser	Phe	Gly	Glu	Met	Lys	Glu	Gly	Ser	Gly	Ser	Gly	Ser	Gly
	130					135					140				
Ser	Ala	Pro	Asp	Val	Gln	Asp	Cys	Pro	Glu	Cys	Thr	Leu	Gln	Glu	Asn
145					150					155				160	
Pro	Phe	Phe	Ser	Gln	Pro	Gly	Ala	Pro	Ile	Leu	Gln	Cys	Met	Gly	Cys
				165					170					175	
Cys	Phe	Ser	Arg	Ala	Tyr	Pro	Thr	Pro	Leu	Arg	Ser	Lys	Lys	Thr	Met
			180					185					190		
Leu	Val	Gln	Lys	Asn	Val	Thr	Ser	Glu	Ser	Thr	Cys	Cys	Val	Ala	Lys
		195					200					205			
Ser	Tyr	Asn	Arg	Val	Thr	Val	Met	Gly	Gly	Phe	Lys	Val	Glu	Asn	His
	210					215					220				
Thr	Ala	Cys	His	Cys	Ser	Thr	Cys	Tyr	Tyr	His	Lys	Ser			

## (2) INFORMATION FOR SEQ ID NO:16:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```

GGTACCTTAA GATTTGTGAT AATAACAAGT ACTGCAGTGG CACGCCGTGT GGTTCTCCAC      60
TTTGAAACCC CCCATTACTG TGACCCTGTT ATATGATTTA GCTACACAGC AAGTGGACTC      120
TGAGGTGACG TTCTTTTGGA CCAACATCGT CTTCTTGGAC CTTAGTGGAG TGGGATATGC      180
TCTAGAGAAG CAGCAGCCCA TGCAGTGAAG TATTGGGGCA CCCGGCTGGG AGAAGAAATGG      240
GTTTTCTGTG AGCGTGCATT CTGGGCAATC CTGCACATCA GGAGCGCTAC CAGATCCGCT      300
ACCGGATCCT TCTTTTCAATT CACCAAAGGA GCAGTAGCTG GGCCCCAGGC CTCGCACAGT      360
ACAATCAGTG CTGTCGCTGT CGCAGAGTGC ACATTGACAG CTGAGAGCCA CGGCGTAGGA      420
GACCACGGGG TTCACGCCGC GCGGGCAGCC AGGGAGCCGG ATGGACTCGA AGCGCACATC      480
GCGGTAGTTG CACACCACCT GAGGCAGGGC CGGCAGGACC CCCTGCAGCA CGCGGGTCAT      540
GGTGGGGCAG TAGCCGGCAC AGATGGTGGT GTTGACGGTG ATGCACACGG GGCAGCCCTC      600
CTTCTCCACA GCCAGGGTGG CATTGATGGG GCGGCACCGT GGCCGAAGCG GCTCCTTGGA      660
TGCCCATGTC CCGCCCATGC TCAGCAGCAG CAACAGCAGC AGCCCCTGGA ACATCTCCAT      720
CCTTGG                                     726

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## (2) INFORMATION FOR SEQ ID NO:17:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 752 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 33...743
- (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```

ATGAAATCGA CGGAATCAGA CTCGAGCCAA GG ATG GAG ATG TTC CAG GGG CTG      53
                               Met Glu Met Phe Gln Gly Leu
                               1             5

CTG CTG TTG CTG CTG CTG AGC ATG GGC GGG ACA TGG GCA TCC AAG GAG      101
Leu Leu Leu Leu Leu Leu Ser Met Gly Gly Thr Trp Ala Ser Lys Glu
    10             15             20

CCG CTT CGG CCA CGG TGC CGC CCC ATC AAT GCC ACC CTG GCT GTG GAG      149
Pro Leu Arg Pro Arg Cys Arg Pro Ile Asn Ala Thr Leu Ala Val Glu
    25             30             35

AAG GAG GGC TGC CCC GTG TGC ATC ACC GTC AAC ACC ACC ATC TGT GCC      197
Lys Glu Gly Cys Pro Val Cys Ile Thr Val Asn Thr Thr Ile Cys Ala

```

40	45	50	55	
GGC TAC TGC CCC ACC ATG ACC CGC GTG CTG CAG GGG GTC CTG CCG GCC				245
Gly Tyr Cys Pro Thr Met Thr Arg Val Leu Gln Gly Val Leu Pro Ala	60	65	70	
CTG CCT CAG GTG GTG TGC AAC TAC CGC GAT GTG CGC TTC GAG TCC ATC				293
Leu Pro Gln Val Val Cys Asn Tyr Arg Asp Val Arg Phe Glu Ser Ile	75	80	85	
CGG CTC CCT GGC TGC CCG CGC GGC GTG AAC CCC GTG GTC TCC TAC GCC				341
Arg Leu Pro Gly Cys Pro Arg Gly Val Asn Pro Val Val Ser Tyr Ala	90	95	100	
GTG GCT CTC AGC TGT CAA TGT GCA CTC TGC CGC CGC AGC ACC ACT GAC				389
Val Ala Leu Ser Cys Gln Cys Ala Leu Cys Arg Arg Ser Thr Thr Asp	105	110	115	
TGC ACT GTG CGA GGC CTG GGG CCC AGC TAC TGC TCC TTT GGT GAA ATG				437
Cys Thr Val Arg Gly Leu Gly Pro Ser Tyr Cys Ser Phe Gly Glu Met	120	125	130	135
AAA GAA GGA TCC GGT AGC GGA TCT GGT AGC GCT CCT GAT GTG CAG GAT				485
Lys Glu Gly Ser Gly Ser Gly Ser Gly Ser Ala Pro Asp Val Gln Asp	140	145	150	
TGC CCA GAA TGC ACG CTA CAG GAA AAC CCA TTC TTC TCC CAG CCG GGT				533
Cys Pro Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly	155	160	165	
GCC CCA ATA CTT CAG TGC ATG GGC TGC TGC TTC TCT AGA GCA TAT CCC				581
Ala Pro Ile Leu Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro	170	175	180	
ACT CCA CTA AGG TCC AAG AAG ACG ATG TTG GTC CAA AAG AAC GTC ACC				629
Thr Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val Thr	185	190	195	
TCA GAG TCC ACT TGC TGT GTA GCT AAA TCA TAT AAC AGG GTC ACA GTA				677
Ser Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val	200	205	210	215
ATG GGG GGT TTC AAA GTG GAG AAC CAC ACG GCG TGC CAC TGC AGT ACT				725
Met Gly Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr	220	225	230	
TGT TAT TAT CAC AAA TCT TAAGGTACC				752
Cys Tyr Tyr His Lys Ser	235			

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 237 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single

76



(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met	Glu	Met	Phe	Gln	Gly	Leu	Leu	Leu	Leu	Leu	Leu	Ser	Met	Gly
1				5				10					15	
Gly	Thr	Trp	Ala	Ser	Lys	Glu	Pro	Leu	Arg	Pro	Arg	Cys	Arg	Ile
			20					25				30		
Asn	Ala	Thr	Leu	Ala	Val	Glu	Lys	Gly	Cys	Pro	Val	Cys	Ile	Thr
		35					40				45			
Val	Asn	Thr	Thr	Ile	Cys	Ala	Gly	Tyr	Cys	Pro	Thr	Met	Thr	Arg
	50					55					60			Val
Leu	Gln	Gly	Val	Leu	Pro	Ala	Leu	Pro	Gln	Val	Val	Cys	Asn	Tyr
65					70				75					80
Asp	Val	Arg	Phe	Glu	Ser	Ile	Arg	Leu	Pro	Gly	Cys	Pro	Arg	Gly
			85						90				95	Val
Asn	Pro	Val	Val	Ser	Tyr	Ala	Val	Ala	Leu	Ser	Cys	Gln	Cys	Ala
			100					105				110		Leu
Cys	Arg	Arg	Ser	Thr	Thr	Asp	Cys	Thr	Val	Arg	Gly	Leu	Gly	Pro
		115					120					125		Ser
Tyr	Cys	Ser	Phe	Gly	Glu	Met	Lys	Glu	Gly	Ser	Gly	Ser	Gly	Ser
	130					135					140			Gly
Ser	Ala	Pro	Asp	Val	Gln	Asp	Cys	Pro	Glu	Cys	Thr	Leu	Gln	Glu
145					150				155					Asn
Pro	Phe	Phe	Ser	Gln	Pro	Gly	Ala	Pro	Ile	Leu	Gln	Cys	Met	Gly
			165					170					175	Cys
Cys	Phe	Ser	Arg	Ala	Tyr	Pro	Thr	Pro	Leu	Arg	Ser	Lys	Lys	Thr
			180					185					190	Met
Leu	Val	Gln	Lys	Asn	Val	Thr	Ser	Glu	Ser	Thr	Cys	Cys	Val	Ala
		195					200					205		Lys
Ser	Tyr	Asn	Arg	Val	Thr	Val	Met	Gly	Gly	Phe	Lys	Val	Glu	Asn
	210						215				220			His
Thr	Ala	Cys	His	Cys	Ser	Thr	Cys	Tyr	Tyr	His	Lys	Ser		
225						230				235				

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 726 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGTACCTTAA	GATTTGTGAT	AATAACAAGT	ACTGCAGTGG	CACGCCGTGT	GGTTCTCCAC	60
TTTGAAACCC	CCCATTACTG	TGACCCTGTT	ATATGATTTA	GCTACACAGC	AAGTGGACTC	120
TGAGGTGACG	TTCTTTTGGG	CCAACATCGT	CTTCTTGGAC	CTTAGTGGAG	TGGGATATGC	180
TCTAGAGAAG	CAGCAGCCCA	TGCACTGAAG	TATTGGGGCA	CCCGGCTGGG	AGAAGATGG	240
GTTTTCTGT	AGCGTGCATT	CTGGGCAATC	CTGCACATCA	GGAGCGCTAC	CAGATCCGCT	300
ACCGGATCCT	TCTTTTATTT	CACCAAAGGA	GCAGTAGCTG	GGCCCCAGGC	CTCGCACAGT	360
GCAGTCAGTG	GTGCTGCGGC	GGCAGAGTGC	ACATTGACAG	CTGAGAGCCA	CGGCGTAGGA	420
GACCACGGGG	TTCACGCCGC	GCGGGCAGCC	AGGGAGCCGG	ATGGACTCGA	AGCGCACATC	480

GCGGTAGTTG	CACACCACCT	GAGGCAGGGC	CGGCAGGACC	CCCTGCAGCA	CGCGGGTCAT	540
GGTGGGGCAG	TAGCCGGCAC	AGATGGTGGT	GTTGACGGTG	ATGCACACGG	GGCAGCCCTC	600
CTTCTCCACA	GCCAGGGTGG	CATTGATGGG	GCGGCACCGT	GGCCGAAGCG	GCTCCTTGGA	660
TGCCCATGTC	CCGCCCATGC	TCAGCAGCAG	CAACAGCAGC	AGCCCCTGGA	ACATCTCCAT	720
CCTTGG						726

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 743 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 33...734
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATGAAATCGA	CGGAATCAGA	CTCGAGCCAA	GG	ATG	GAG	ATG	TTC	CAG	GGG	CTG	53					
				Met	Glu	Met	Phe	Gln	Gly	Leu						
				1				5								
CTG	CTG	TTG	CTG	CTG	CTG	AGC	ATG	GGC	GGG	ACA	TGG	GCA	TCC	AAG	GAG	101
Leu	Leu	Leu	Leu	Leu	Leu	Ser	Met	Gly	Gly	Thr	Trp	Ala	Ser	Lys	Glu	
		10					15					20				
CCG	CTT	CGG	CCA	CGG	TGC	CGC	CCC	ATC	AAT	GCC	ACC	CTG	GCT	GTG	GAG	149
Pro	Leu	Arg	Pro	Arg	Cys	Arg	Pro	Ile	Asn	Ala	Thr	Leu	Ala	Val	Glu	
	25					30					35					
AAG	GAG	GGC	TGC	CCC	GTG	TGC	ATC	ACC	GTC	AAC	ACC	ACC	ATC	TGT	GCC	197
Lys	Glu	Gly	Cys	Pro	Val	Cys	Ile	Thr	Val	Asn	Thr	Thr	Ile	Cys	Ala	
40					45				50						55	
GGC	TAC	TGC	CCC	ACC	ATG	ACC	CGC	GTG	CTG	CAG	GGG	GTC	CTG	CCG	GCC	245
Gly	Tyr	Cys	Pro	Thr	Met	Thr	Arg	Val	Leu	Gln	Gly	Val	Leu	Pro	Ala	
				60					65					70		
CTG	CCT	CAG	GTG	GTG	TGC	AAC	TAC	CGC	GAT	GTG	CGC	TTC	GAG	TCC	ATC	293
Leu	Pro	Gln	Val	Val	Cys	Asn	Tyr	Arg	Asp	Val	Arg	Phe	Glu	Ser	Ile	
			75					80					85			
CGG	CTC	CCT	GGC	TGC	CCG	CGC	GGC	GTG	AAC	CCC	GTG	GTC	TCC	TAC	GCC	341
Arg	Leu	Pro	Gly	Cys	Pro	Arg	Gly	Val	Asn	Pro	Val	Val	Ser	Tyr	Ala	
		90					95					100				
GTG	GCT	CTC	AGC	TGT	CAA	TGT	GCA	CTC	TGC	CGC	CGC	AGC	ACC	ACT	GAC	389
Val	Ala	Leu	Ser	Cys	Gln	Cys	Ala	Leu	Cys	Arg	Arg	Ser	Thr	Thr	Asp	
	105					110					115					
TGC	ACT	GTG	CGA	GGC	CTG	GGG	CCC	AGC	TAC	TGC	TCC	TTT	GGT	GAA	GGA	437
Cys	Thr	Val	Arg	Gly	Leu	Gly	Pro	Ser	Tyr	Cys	Ser	Phe	Gly	Glu	Gly	
120					125					130					135	

78

TCC GGT AGC GGA TCT GGT AGC GCT CCT GAT GTG CAG GAT TGC CCA GAA	485
Ser Gly Ser Gly Ser Gly Ser Ala Pro Asp Val Gln Asp Cys Pro Glu	
140 145 150	
TGC ACG CTA CAG GAA AAC CCA TTC TTC TCC CAG CCG GGT GCC CCA ATA	533
Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile	
155 160 165	
CTT CAG TGC ATG GGC TGC TGC TTC TCT AGA GCA TAT CCC ACT CCA CTA	581
Leu Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro Leu	
170 175 180	
AGG TCC AAG AAG ACG ATG TTG GTC CAA AAG AAC GTC ACC TCA GAG TCC	629
Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser Glu Ser	
185 190 195	
ACT TGC TGT GTA GCT AAA TCA TAT AAC AGG GTC ACA GTA ATG GGG GGT	677
Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met Gly Gly	
200 205 210 215	
TTC AAA GTG GAG AAC CAC ACG GCG TGC CAC TGC AGT ACT TGT TAT TAT	725
Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr Tyr	
220 225 230	
CAC AAA TCT TAAGGTACC	743
His Lys Ser	

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Glu Met Phe Gln Gly Leu Leu Leu Leu Leu Leu Ser Met Gly	
1 5 10 15	
Gly Thr Trp Ala Ser Lys Glu Pro Leu Arg Pro Arg Cys Arg Pro Ile	
20 25 30	
Asn Ala Thr Leu Ala Val Glu Lys Glu Gly Cys Pro Val Cys Ile Thr	
35 40 45	
Val Asn Thr Thr Ile Cys Ala Gly Tyr Cys Pro Thr Met Thr Arg Val	
50 55 60	
Leu Gln Gly Val Leu Pro Ala Leu Pro Gln Val Val Cys Asn Tyr Arg	
65 70 75 80	
Asp Val Arg Phe Glu Ser Ile Arg Leu Pro Gly Cys Pro Arg Gly Val	
85 90 95	
Asn Pro Val Val Ser Tyr Ala Val Ala Leu Ser Cys Gln Cys Ala Leu	
100 105 110	

Cys Arg Arg Ser Thr Thr Asp Cys Thr Val Arg Gly Leu Gly Pro Ser  
 115 120 125  
 Tyr Cys Ser Phe Gly Glu Gly Ser Gly Ser Gly Ser Gly Ser Ala Pro  
 130 135 140  
 Asp Val Gln Asp Cys Pro Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe  
 145 150 155 160  
 Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys Met Gly Cys Cys Phe Ser  
 165 170 175  
 Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln  
 180 185 190  
 Lys Asn Val Thr Ser Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn  
 195 200 205  
 Arg Val Thr Val Met Gly Gly Phe Lys Val Glu Asn His Thr Ala Cys  
 210 215 220  
 His Cys Ser Thr Cys Tyr Tyr His Lys Ser  
 225 230

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 717 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GGTACCTTAA	GATTTGTGAT	AATAACAAGT	ACTGCAGTGG	CACGCCGTGT	GGTTCTCCAC	60
TTTGAAACCC	CCCATTACTG	TGACCCTGTT	ATATGATTTA	GCTACACAGC	AAGTGGACTC	120
TGAGGTGACG	TTCTTTTGGG	CCAACATCGT	CTTCTTGGAC	CTTAGTGGAG	TGGGATATGC	180
TCTAGAGAAG	CAGCAGCCCA	TGCACTGAAG	TATTGGGGCA	CCCGGCTGGG	AGAAGAATGG	240
GTTTTCTGT	AGCGTGCATT	CTGGGCAATC	CTGCACATCA	GGAGCGCTAC	CAGATCCGCT	300
ACCGGATCCT	TCACCAAAGG	AGCAGTAGCT	GGGCCCCAGG	CCTCGCACAG	TGCAGTCAGT	360
GGTGCTGCGG	CGGCAGAGTG	CACATTGACA	GCTGAGAGCC	ACGGCGTAGG	AGACCACGGG	420
GTTACGCGCG	CGCGGGCAGC	CAGGGAGCCG	GATGGACTCG	AAGCGCACAT	CGCGGTAGTT	480
GCACACCACC	TGAGGCAGGG	CCGGCAGGAC	CCCCTGCAGC	ACGCGGGTCA	TGGTGGGGCA	540
GTAGCCGGCA	CAGATGGTGG	TGTTGACGGT	GATGCACACG	GGGCAGCCCT	CCTTCTCCAC	600
AGCCAGGGTG	GCATTGATGG	GGCGGCACCG	TGGCCGAAGC	GGCTCCTTGG	ATGCCCATGT	660
CCCGCCCATG	CTCAGCAGCA	GCAACAGCAG	CAGCCCCTGG	AACATCTCCA	TCCTTGG	717

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 743 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 33...734
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

80

ATGAAATCGA CGGAATCAGA CTCGAGCCAA GG	ATG Met 1	GAG Glu	ATG Met	TTC Phe	CAG Gln	GGG Gly	CTG Leu	53
CTG CTG TTG CTG CTG CTG AGC ATG GGC GGG ACA TGG GCA TCC AAG GAG	Leu 10	Leu 10	Leu 10	Leu 10	Leu 10	Ser 15	Met 15	101
CCG CTT CGG CCA CGG TGC CGC CCC ATC AAT GCC ACC CTG GCT GTG GAG	Pro 25	Leu 25	Arg 25	Pro 25	Arg 25	Cys 30	Arg 30	149
AAG GAG GGC TGC CCC GTG TGC ATC ACC GTC AAC ACC ACC ATC TGT GCC	Lys 40	Glu 40	Gly 40	Cys 45	Pro 45	Val 45	Cys 45	197
GGC TAC TGC CCC ACC ATG ACC CGC GTG CTG CAG GGG GTC CTG CCG GCC	Gly 60	Tyr 60	Cys 60	Pro 60	Thr 60	Met 60	Thr 65	245
CTG CCT CAG GTG GTG TGC AAC TAC CGC GAT GTG CGC TTC GAG TCC ATC	Leu 75	Pro 75	Gln 75	Val 75	Val 75	Cys 75	Asn 80	293
CGG CTC CCT GGC TGC CCG CGC GGC GTG AAC CCC GTG GTC TCC TAC GCC	Arg 90	Leu 90	Pro 90	Gly 90	Cys 90	Pro 95	Arg 95	341
GTG GCT CTC AGC TGT CAA TGT GCA CTC TGC CGC CGC AGC ACC ACT GAC	Val 105	Ala 105	Leu 105	Ser 105	Cys 105	Gln 110	Cys 110	389
TGC ACT GTG CGA GGC CTG GGG CCC AGC TAC TGC GAT GAC CCG CGG GGA	Cys 120	Thr 120	Val 120	Arg 120	Gly 125	Leu 125	Gly 130	437
TCC GGT AGC GGA TCT GGT AGC GCT CCT GAT GTG CAG GAT TGC CCA GAA	Ser 140	Gly 140	Ser 140	Gly 140	Ser 140	Gly 140	Ala 145	485
TGC ACG CTA CAG GAA AAC CCA TTC TTC TCC CAG CCG GGT GCC CCA ATA	Cys 155	Thr 155	Leu 155	Gln 155	Glu 155	Asn 155	Pro 160	533
CTT CAG TGC ATG GGC TGC TGC TTC TCT AGA GCA TAT CCC ACT CCA CTA	Leu 170	Gln 170	Cys 170	Met 170	Gly 170	Cys 175	Cys 175	581
AGG TCC AAG AAG ACG ATG TTG GTC CAA AAG AAC GTC ACC TCA GAG TCC	Arg 185	Ser 185	Lys 185	Lys 185	Thr 185	Met 190	Leu 190	629
ACT TGC TGT GTA GCT AAA TCA TAT AAC AGG GTC ACA GTA ATG GGG GGT	Thr 200	Cys 200	Cys 200	Val 200	Ala 205	Lys 205	Ser 210	677
TTC AAA GTG GAG AAC CAC ACG GCG TGC CAC TGC AGT ACT TGT TAT TAT								725

81

Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr Tyr  
 220 225 230

CAC AAA TCT TAAGGTACC  
 His Lys Ser

743

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met	Glu	Met	Phe	Gln	Gly	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Ser	Met	Gly
1				5				10					15		
Gly	Thr	Trp	Ala	Ser	Lys	Glu	Pro	Leu	Arg	Pro	Arg	Cys	Arg	Pro	Ile
			20				25					30			
Asn	Ala	Thr	Leu	Ala	Val	Glu	Lys	Glu	Gly	Cys	Pro	Val	Cys	Ile	Thr
		35				40					45				
Val	Asn	Thr	Thr	Ile	Cys	Ala	Gly	Tyr	Cys	Pro	Thr	Met	Thr	Arg	Val
	50				55				60						
Leu	Gln	Gly	Val	Leu	Pro	Ala	Leu	Pro	Gln	Val	Val	Cys	Asn	Tyr	Arg
65				70				75						80	
Asp	Val	Arg	Phe	Glu	Ser	Ile	Arg	Leu	Pro	Gly	Cys	Pro	Arg	Gly	Val
			85					90						95	
Asn	Pro	Val	Val	Ser	Tyr	Ala	Val	Ala	Leu	Ser	Cys	Gln	Cys	Ala	Leu
		100					105					110			
Cys	Arg	Arg	Ser	Thr	Thr	Asp	Cys	Thr	Val	Arg	Gly	Leu	Gly	Pro	Ser
	115					120					125				
Tyr	Cys	Asp	Asp	Pro	Arg	Gly	Ser	Gly	Ser	Gly	Ser	Gly	Ser	Ala	Pro
	130					135				140					
Asp	Val	Gln	Asp	Cys	Pro	Glu	Cys	Thr	Leu	Gln	Glu	Asn	Pro	Phe	Phe
145				150				155						160	
Ser	Gln	Pro	Gly	Ala	Pro	Ile	Leu	Gln	Cys	Met	Gly	Cys	Cys	Phe	Ser
			165				170							175	
Arg	Ala	Tyr	Pro	Thr	Pro	Leu	Arg	Ser	Lys	Lys	Thr	Met	Leu	Val	Gln
		180				185						190			
Lys	Asn	Val	Thr	Ser	Glu	Ser	Thr	Cys	Cys	Val	Ala	Lys	Ser	Tyr	Asn
	195					200					205				
Arg	Val	Thr	Val	Met	Gly	Gly	Phe	Lys	Val	Glu	Asn	His	Thr	Ala	Cys
	210				215					220					
His	Cys	Ser	Thr	Cys	Tyr	Tyr	His	Lys	Ser						
225				230											

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 717 base pairs
- (B) TYPE: nucleic acid

82

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GGTACCTTAA	GATTTGTGAT	AATAACAAGT	ACTGCAGTGG	CACGCCGTGT	GGTTCTCCAC	60
TTTGAAACCC	CCCATTACTG	TGACCCTGTT	ATATGATTTA	GCTACACAGC	AAGTGGACTC	120
TGAGGTGACG	TTCTTTTGA	CCAACATCGT	CTTCTTGAC	CTTAGTGGAG	TGGGATATGC	180
TCTAGAGAAG	CAGCAGCCCA	TGCACTGAAG	TATTGGGGCA	CCCGGCTGGG	AGAAGAATGG	240
GTTTTCTGT	AGCGTGCATT	CTGGGCAATC	CTGCACATCA	GGAGCGCTAC	CAGATCCGCT	300
ACCGGATCCC	CGCGGGTCAT	CGCAGTAGCT	GGGCCCCAGG	CCTCGCACAG	TGCAGTCAGT	360
GGTGCTGCGG	CGGCAGAGTG	CACATTGACA	GCTGAGAGCC	ACGGCGTAGG	AGACCACGGG	420
GTTCACGCCG	CGCGGGCAGC	CAGGGAGCCG	GATGGACTCG	AAGCGCACAT	CGCGGTAGTT	480
GCACACCACC	TGAGGCAGGG	CCGGCAGGAC	CCCCTGCAGC	ACGCGGGTCA	TGGTGGGGCA	540
GTAGCCGGCA	CAGATGGTGG	TGTTGACGGT	GATGCACACG	GGGCAGCCCT	CCTTCTCCAC	600
AGCCAGGGTG	GCATTGATGG	GGCGGCACCG	TGGCCGAAGC	GGCTCCTTGG	ATGCCCATGT	660
CCCGCCCATG	CTCAGCAGCA	GCAACAGCAG	CAGCCCCTGG	AACATCTCCA	TCCTTGG	717

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 719 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
(B) LOCATION: 33...700  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ATGAAATCGA	CGGAATCAGA	CTCGAGCCAA	GG	ATG	AAG	ACA	CTC	CAG	TTT	TTC	53
				Met	Lys	Thr	Leu	Gln	Phe	Phe	
				1				5			
TTC	CTT	TTC	TGT	TGC	TGG	AAA	GCA	ATC	TGC	TGC	101
Phe	Leu	Phe	Cys	Cys	Trp	Lys	Ala	Ile	Cys	Cys	
	10					15				20	
ACC	AAC	ATC	ACC	ATT	GCA	ATA	GAG	AAA	GAA	GAA	149
Thr	Asn	Ile	Thr	Ile	Ala	Ile	Glu	Lys	Glu	Glu	
	25				30				35		
AGC	ATC	AAC	ACC	ACT	TGG	TGT	GCT	GGC	TAC	TGC	197
Ser	Ile	Asn	Thr	Thr	Trp	Cys	Ala	Gly	Tyr	Cys	
	40				45			50		55	
GTG	TAT	AAG	GAC	CCA	GCC	AGG	CCC	AAA	ATC	CAG	245
Val	Tyr	Lys	Asp	Pro	Ala	Arg	Pro	Lys	Ile	Gln	
				60				65			
AAG	GAA	CTG	GTA	TAT	GAA	ACA	GTG	AGA	GTG	CCC	293
Lys	Glu	Leu	Val	Tyr	Glu	Thr	Val	Arg	Val	Pro	

83

75										80					85					
GCA	GAT	TCC	TTG	TAT	ACA	TAC	CCA	GTG	GCC	ACC	CAG	TGT	CAC	TGT	GGC	341				
Ala	Asp	Ser	Leu	Tyr	Thr	Tyr	Pro	Val	Ala	Thr	Gln	Cys	His	Cys	Gly					
90						95						100								
AAG	TGT	GAC	AGC	GAC	AGC	ACT	GAT	TGT	ACT	GTG	CGA	GGC	CTG	GGG	CCC	389				
Lys	Cys	Asp	Ser	Asp	Ser	Thr	Asp	Cys	Thr	Val	Arg	Gly	Leu	Gly	Pro					
105						110						115								
AGC	TAC	TGC	TCC	TTT	GGT	GAA	GGA	TCC	GGT	AGC	GGA	TCT	GGT	AGC	GCT	437				
Ser	Tyr	Cys	Ser	Phe	Gly	Glu	Gly	Ser	Gly	Ser	Gly	Ser	Gly	Ser	Ala					
120			125						130			135								
CCT	GAT	GTG	CAG	GAT	TGC	CCA	GAA	TGC	ACG	CTA	CAG	GAA	AAC	CCA	TTC	485				
Pro	Asp	Val	Gln	Asp	Cys	Pro	Glu	Cys	Thr	Leu	Gln	Glu	Asn	Pro	Phe					
			140						145			150								
TTC	TCC	CAG	CCG	GGT	GCC	CCA	ATA	CTT	CAG	TGC	ATG	GGC	TGC	TGC	TTC	533				
Phe	Ser	Gln	Pro	Gly	Ala	Pro	Ile	Leu	Gln	Cys	Met	Gly	Cys	Cys	Phe					
			155			160						165								
TCT	AGA	GCA	TAT	CCC	ACT	CCA	CTA	AGG	TCC	AAG	AAG	ACG	ATG	TTG	GTC	581				
Ser	Arg	Ala	Tyr	Pro	Thr	Pro	Leu	Arg	Ser	Lys	Lys	Thr	Met	Leu	Val					
170						175						180								
CAA	AAG	AAC	GTC	ACC	TCA	GAG	TCC	ACT	TGC	TGT	GTA	GCT	AAA	TCA	TAT	629				
Gln	Lys	Asn	Val	Thr	Ser	Glu	Ser	Thr	Cys	Cys	Val	Ala	Lys	Ser	Tyr					
185						190						195								
AAC	AGG	GTC	ACA	GTA	ATG	GGG	GGT	TTC	AAA	GTG	GAG	AAC	CAC	ACG	GCG	677				
Asn	Arg	Val	Thr	Val	Met	Gly	Gly	Phe	Lys	Val	Glu	Asn	His	Thr	Ala					
200			205						210			215								
TGC	CAC	TGC	AGT	ACT	TGT	TAT	TA	TCACAAATCT	TAAGGTACC							719				
Cys	His	Cys	Ser	Thr	Cys	Tyr	Tyr													
			220																	

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met	Lys	Thr	Leu	Gln	Phe	Phe	Phe	Leu	Phe	Cys	Cys	Trp	Lys	Ala	Ile
1				5					10					15	
Cys	Cys	Asn	Ser	Cys	Glu	Leu	Thr	Asn	Ile	Thr	Ile	Ala	Ile	Glu	Lys
		20						25					30		
Glu	Glu	Cys	Arg	Phe	Cys	Ile	Ser	Ile	Asn	Thr	Thr	Trp	Cys	Ala	Gly

84





(A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 33...698  
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ATGAAATCGA CGGAATCAGA CTCGAGCCAA GG ATG AAG ACA CTC CAG TTT TTC	53
Met Lys Thr Leu Gln Phe Phe	
1 5	
TTC CTT TTC TGT TGC TGG AAA GCA ATC TGC TGC AAT AGC TGT GAG CTG	101
Phe Leu Phe Cys Cys Trp Lys Ala Ile Cys Cys Asn Ser Cys Glu Leu	
10 15 20	
ACC AAC ATC ACC ATT GCA ATA GAG AAA GAA GAA TGT CGT TTC TGC ATA	149
Thr Asn Ile Thr Ile Ala Ile Glu Lys Glu Glu Cys Arg Phe Cys Ile	
25 30 35	
AGC ATC AAC ACC ACT TGG TGT GCT GGC TAC TGC TAC ACC AGG GAT CTG	197
Ser Ile Asn Thr Thr Trp Cys Ala Gly Tyr Cys Tyr Thr Arg Asp Leu	
40 45 50 55	
GTG TAT AAG GAC CCA GCC AGG CCC AAA ATC CAG AAA ACA TGT ACC TTC	245
Val Tyr Lys Asp Pro Ala Arg Pro Lys Ile Gln Lys Thr Cys Thr Phe	
60 65 70	
AAG GAA CTG GTA TAT GAA ACA GTG AGA GTG CCC GGC TGT GCT CAC CAT	293
Lys Glu Leu Val Tyr Glu Thr Val Arg Val Pro Gly Cys Ala His His	
75 80 85	
GCA GAT TCC TTG TAT ACA TAC CCA GTG GCC ACC CAG TGT CAC TGT GGC	341
Ala Asp Ser Leu Tyr Thr Tyr Pro Val Ala Thr Gln Cys His Cys Gly	
90 95 100	
AAG TGT GAC AGC GAC AGC ACT GAT TGT ACT GTG CGA GGC CTG GGG CCC	389
Lys Cys Asp Ser Asp Ser Thr Asp Cys Thr Val Arg Gly Leu Gly Pro	
105 110 115	
AGC TAC TGC GGA TCC GGT AGC GGA TCT GGT AGC GCT CCT GAT GTG CAG	437
Ser Tyr Cys Gly Ser Gly Ser Gly Ser Gly Ser Ala Pro Asp Val Gln	
120 125 130 135	
GAT TGC CCA GAA TGC ACG CTA CAG GAA AAC CCA TTC TTC TCC CAG CCG	485
Asp Cys Pro Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro	
140 145 150	
GGT GCC CCA ATA CTT CAG TGC ATG GGC TGC TGC TTC TCT AGA GCA TAT	533
Gly Ala Pro Ile Leu Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr	
155 160 165	
CCC ACT CCA CTA AGG TCC AAG AAG ACG ATG TTG GTC CAA AAG AAC GTC	581
Pro Thr Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val	
170 175 180	
ACC TCA GAG TCC ACT TGC TGT GTA GCT AAA TCA TAT AAC AGG GTC ACA	629
Thr Ser Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr	

820

185		190		195	
GTA ATG GGG GGT TTC AAA GTG GAG AAC CAC ACG GCG TGC CAC TGC AGT					677
Val Met Gly Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser					
200		205		210	215
ACT TGT TAT TAT CAC AAA TCT TAAGGTACC					707
Thr Cys Tyr Tyr His Lys Ser					
220					

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met	Lys	Thr	Leu	Gln	Phe	Phe	Phe	Leu	Phe	Cys	Cys	Trp	Lys	Ala	Ile
1			5					10					15		
Cys	Cys	Asn	Ser	Cys	Glu	Leu	Thr	Asn	Ile	Thr	Ile	Ala	Ile	Glu	Lys
		20					25					30			
Glu	Glu	Cys	Arg	Phe	Cys	Ile	Ser	Ile	Asn	Thr	Thr	Trp	Cys	Ala	Gly
		35				40					45				
Tyr	Cys	Tyr	Thr	Arg	Asp	Leu	Val	Tyr	Lys	Asp	Pro	Ala	Arg	Pro	Lys
	50				55					60					
Ile	Gln	Lys	Thr	Cys	Thr	Phe	Lys	Glu	Leu	Val	Tyr	Glu	Thr	Val	Arg
65				70				75						80	
Val	Pro	Gly	Cys	Ala	His	His	Ala	Asp	Ser	Leu	Tyr	Thr	Tyr	Pro	Val
			85					90						95	
Ala	Thr	Gln	Cys	His	Cys	Gly	Lys	Cys	Asp	Ser	Asp	Ser	Thr	Asp	Cys
		100					105						110		
Thr	Val	Arg	Gly	Leu	Gly	Pro	Ser	Tyr	Cys	Gly	Ser	Gly	Ser	Gly	Ser
		115				120						125			
Gly	Ser	Ala	Pro	Asp	Val	Gln	Asp	Cys	Pro	Glu	Cys	Thr	Leu	Gln	Glu
	130				135				140						
Asn	Pro	Phe	Phe	Ser	Gln	Pro	Gly	Ala	Pro	Ile	Leu	Gln	Cys	Met	Gly
145				150					155					160	
Cys	Cys	Phe	Ser	Arg	Ala	Tyr	Pro	Thr	Pro	Leu	Arg	Ser	Lys	Lys	Thr
			165					170						175	
Met	Leu	Val	Gln	Lys	Asn	Val	Thr	Ser	Glu	Ser	Thr	Cys	Cys	Val	Ala
		180					185					190			
Lys	Ser	Tyr	Asn	Arg	Val	Thr	Val	Met	Gly	Gly	Phe	Lys	Val	Glu	Asn
		195				200						205			
His	Thr	Ala	Cys	His	Cys	Ser	Thr	Cys	Tyr	Tyr	His	Lys	Ser		
	210				215						220				

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 681 base pairs

87

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GGTACCTTAA	GATTTGTGAT	AATAACAAGT	ACTGCAGTGG	CACGCCGTGT	GGTTCTCCAC	60
TTTGAAACCC	CCCATTACTG	TGACCCTGTT	ATATGATTTA	GCTACACAGC	AAGTGGACTC	120
TGAGGTGACG	TTCTTTTGGG	CCAACATCGT	CTTCTTGGAC	CTTAGTGGAG	TGGGATATGC	180
TCTAGAGAAG	CAGCAGCCCA	TGCACTGAAG	TATTGGGGCA	CCCGGCTGGG	AGAAGAATGG	240
GTTTTCTGT	AGCGTGCATT	CTGGGCAATC	CTGCACATCA	GGAGCGCTAC	CAGATCCGCT	300
ACCGGATCCG	CAGTAGCTGG	GCCCCAGGCC	TCGCACAGTA	CAATCAGTGC	TGTCGCTGTC	360
ACACTTGCCA	CAGTGACACT	GGGTGGCCAC	TGGGTATGTA	TACAAGGAAT	CTGCATGGTG	420
AGCACAGCCG	GGCACTCTCA	CTGTTTCATA	TACCAGTTCC	TTGAAGGTAC	ATGTTTTCTG	480
GATTTTGGGC	CTGGCTGGGT	CCTTATACAC	CAGATCCCTG	GTGTAGCAGT	AGCCAGCACA	540
CCAAGTGGTG	TTGATGCTTA	TGCAGAAACG	ACATTCTTCT	TTCTCTATTG	CAATGGTGAT	600
GTTGGTCAGC	TCACAGCTAT	TGCAGCAGAT	TGCTTTCCAG	CAACAGAAAA	GGAAGAAAAA	660
CTGGAGTGTC	TTCATCCTTG	G				681

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...303
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TGC GGA TCC GGT AGC GGA TCT GGT AGC GCT CCT GAT GTG CAG GAT TGC	48
Cys Gly Ser Gly Ser Gly Ser Gly Ser Ala Pro Asp Val Gln Asp Cys	
1 5 10 15	
CCA GAA TGC ACG CTA CAG GAA AAC CCA TTC TTC TCC CAG CCG GGT GCC	96
Pro Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala	
20 25 30	
CCA ATA CTT CAG TGC ATG GGC TGC TGC TTC TCT AGA GCA TAT CCC ACT	144
Pro Ile Leu Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr	
35 40 45	
CCA CTA AGG TCC AAG AAG ACG ATG TTG GTC CAA AAG CAA GTC ACC TCA	192
Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Gln Val Thr Ser	
50 55 60	
GAG TCC ACT TGC TGT GTA GCT AAA TCA TAT AAC AGG GTC ACA GTA ATG	240
Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met	
65 70 75 80	
GGG GGT TTC AAA GTG GAG CAA CAC ACG GCG TGC CAC TGC AGT ACT TGT	288

88

Gly Gly Phe Lys Val Glu Gln His Thr Ala Cys His Cys Ser Thr Cys  
85 90 95

TAT TAT CAC AAA TCT TAAGGTACC  
Tyr Tyr His Lys Ser  
100

312

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Cys	Gly	Ser	Gly	Ser	Gly	Ser	Gly	Ser	Ala	Pro	Asp	Val	Gln	Asp	Cys
1				5					10					15	
Pro	Glu	Cys	Thr	Leu	Gln	Glu	Asn	Pro	Phe	Phe	Ser	Gln	Pro	Gly	Ala
			20					25					30		
Pro	Ile	Leu	Gln	Cys	Met	Gly	Cys	Cys	Phe	Ser	Arg	Ala	Tyr	Pro	Thr
		35					40					45			
Pro	Leu	Arg	Ser	Lys	Lys	Thr	Met	Leu	Val	Gln	Lys	Gln	Val	Thr	Ser
	50					55					60				
Glu	Ser	Thr	Cys	Cys	Val	Ala	Lys	Ser	Tyr	Asn	Arg	Val	Thr	Val	Met
65					70					75					80
Gly	Gly	Phe	Lys	Val	Glu	Gln	His	Thr	Ala	Cys	His	Cys	Ser	Thr	Cys
			85						90					95	
Tyr	Tyr	His	Lys	Ser											
			100												

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GTACCGGTAC	CTTAAGATTT	GTGATAATAA	CAAGTACTGC	AGTGGCACGC	CGTGTGTTGC	60
TCCACTTTGA	AACCCCCCAT	TACTGTGACC	CTGTTATATG	ATTTAGCTAC	ACAGCAAGTG	120
GACTCTGAGG	TGACTTGCTT	TTGGACCAAC	ATCGTCTTCT	TGGACCTTAG	TGGAGTGGGA	180
TATGCTCTAG	AGAAGCAGCA	GCCCATGCAC	TGAAGTATTG	GGGCACCCGG	CTGGGAGAAG	240
AATGGGTTTT	CCTGTAGCGT	GCATTCTGGG	CAATCCTGCA	CATCAGGAGC	GCTACCAGAT	300
CCGCTACCGG	ATCCGCA					317

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:



(A) LENGTH: 575 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 33...575  
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ATGAAATCGA CGGAATCAGA CTCGAGCCAA GG	ATG GAG ATG TTC CAG GGG CTG	53
	Met Glu Met Phe Gln Gly Leu	
	1 5	
CTG CTG TTG CTG CTG CTG AGC ATG GGC GGG ACA TGG GCA TCC AAG GAG		101
Leu Leu Leu Leu Leu Leu Ser Met Gly Gly Thr Trp Ala Ser Lys Glu		
10 15 20		
CCG CTT CGG CCA CGG TGC CGC CCC ATC CAA GCC ACC CTG GCT GTG GAG		149
Pro Leu Arg Pro Arg Cys Arg Pro Ile Gln Ala Thr Leu Ala Val Glu		
25 30 35		
AAG GAG GGC TGC CCC GTG TGC ATC ACC GTC AAC ACC ACC ATC TGT GCC		197
Lys Glu Gly Cys Pro Val Cys Ile Thr Val Asn Thr Thr Ile Cys Ala		
40 45 50 55		
GGC TAC TGC CCC ACC ATG ACC CGC GTG CTG CAG GGG GTC CTG CCG GCC		245
Gly Tyr Cys Pro Thr Met Thr Arg Val Leu Gln Gly Val Leu Pro Ala		
60 65 70		
CTG CCT CAG GTG GTG TGC AAC TAC CGC GAT GTG CGC TTC GAG TCC ATC		293
Leu Pro Gln Val Val Cys Asn Tyr Arg Asp Val Arg Phe Glu Ser Ile		
75 80 85		
CGG CTC CCT GGC TGC CCG CGC GGC GTG AAC CCC GTG GTC TCC TAC GCC		341
Arg Leu Pro Gly Cys Pro Arg Gly Val Asn Pro Val Val Ser Tyr Ala		
90 95 100		
GTG GCT CTC AGC TGT CAA TGT GCA CTC TGC CGC CGC AGC ACC ACT GAC		389
Val Ala Leu Ser Cys Gln Cys Ala Leu Cys Arg Arg Ser Thr Thr Asp		
105 110 115		
TGC GGG GGT CCC AAG GAC CAC CCC TTG ACC TGT GAT GAC CCC CGC TTC		437
Cys Gly Gly Pro Lys Asp His Pro Leu Thr Cys Asp Asp Pro Arg Phe		
120 125 130 135		
CAG GAC TCC TCT TCC TCA AAG GCC CCT CCC CCC AGC CTT CCA AGC CCA		485
Gln Asp Ser Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu Pro Ser Pro		
140 145 150		
TCC CGA CTC CCG GGG CCC TCG GAC ACC CCG ATC CTC CCC CAA GGA TCC		533
Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro Gln Gly Ser		
155 160 165		

GGT AGC GGA TCT GGT AGC GCT CCT GAT GTG CAG GAT TGC CCA  
 Gly Ser Gly Ser Gly Ser Ala Pro Asp Val Gln Asp Cys Pro  
 170 175 180

575

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met	Glu	Met	Phe	Gln	Gly	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Ser	Met	Gly
1				5					10					15	
Gly	Thr	Trp	Ala	Ser	Lys	Glu	Pro	Leu	Arg	Pro	Arg	Cys	Arg	Pro	Ile
			20					25					30		
Gln	Ala	Thr	Leu	Ala	Val	Glu	Lys	Glu	Gly	Cys	Pro	Val	Cys	Ile	Thr
			35				40					45			
Val	Asn	Thr	Thr	Ile	Cys	Ala	Gly	Tyr	Cys	Pro	Thr	Met	Thr	Arg	Val
	50					55					60				
Leu	Gln	Gly	Val	Leu	Pro	Ala	Leu	Pro	Gln	Val	Val	Cys	Asn	Tyr	Arg
65					70				75					80	
Asp	Val	Arg	Phe	Glu	Ser	Ile	Arg	Leu	Pro	Gly	Cys	Pro	Arg	Gly	Val
			85					90						95	
Asn	Pro	Val	Val	Ser	Tyr	Ala	Val	Ala	Leu	Ser	Cys	Gln	Cys	Ala	Leu
			100					105					110		
Cys	Arg	Arg	Ser	Thr	Thr	Asp	Cys	Gly	Gly	Pro	Lys	Asp	His	Pro	Leu
			115				120					125			
Thr	Cys	Asp	Asp	Pro	Arg	Phe	Gln	Asp	Ser	Ser	Ser	Ser	Lys	Ala	Pro
	130					135					140				
Pro	Pro	Ser	Leu	Pro	Ser	Pro	Ser	Arg	Leu	Pro	Gly	Pro	Ser	Asp	Thr
145					150				155					160	
Pro	Ile	Leu	Pro	Gln	Gly	Ser	Gly	Ser	Gly	Ser	Gly	Ser	Ala	Pro	Asp
				165			170							175	
Val	Gln	Asp	Cys	Pro											
			180												

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

TGGGCAATCC	TGCACATCAG	GAGCGCTACC	AGATCCGCTA	CCGGATCCTT	GGGGGAGGAT	60
CGGGGTGTCC	GAGGGCCCCG	GGAGTCGGGA	TGGGCTTGGA	AGGCTGGGGG	GAGGGGCCCTT	120
TGAGGAAGAG	GAGTCCTGGA	AGCGGGGGTC	ATCACAGGTC	AAGGGGTGGT	CCTTGGGACC	180

CCCGCAGTCA	GTGGTGCTGC	GGCGGCAGAG	TGCACATTGA	CAGCTGAGAG	CCACGGCGTA	240
GGAGACCACG	GGGTTCACGC	CGCGCGGGCA	GCCAGGGAGC	CGGATGGACT	CGAAGCGCAC	300
ATCGCGGTAG	TTGCACACCA	CCTGAGGCAG	GGCCGGCAGG	ACCCCTGCA	GCACGCGGGT	360
CATGGTGGGG	CAGTAGCCGG	CACAGATGGT	GGTGTGACG	GTGATGCACA	CGGGGCAGCC	420
CTCCTTCTCC	ACAGCCAGGG	TGGCTTGGAT	GGGGCGGCAC	CGTGGCCGAA	GCGGCTCCTT	480
GGATGCCCCAT	GTCCCCGCCA	TGCTCAGCAG	CAGCAACAGC	AGCAGCCCCT	GGAACATCTC	540
CATCCTTGG						549

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 837 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 33...827
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

ATGAAATCGA	CGGAATCAGA	CTCGAGCCAA	GG	ATG	GAG	ATG	TTC	CAG	GGG	CTG	53
				Met	Glu	Met	Phe	Gln	Gly	Leu	
				1				5			
CTG	CTG	TTG	CTG	CTG	CTG	AGC	ATG	GGC	GGG	ACA	101
Leu	Leu	Leu	Leu	Leu	Leu	Ser	Met	Gly	Gly	Thr	
		10					15			20	
CCG	CTT	CGG	CCA	CGG	TGC	CGC	CCC	ATC	AAT	GCC	149
Pro	Leu	Arg	Pro	Arg	Cys	Arg	Pro	Ile	Asn	Ala	
	25				30					35	
AAG	GAG	GGC	TGC	CCC	GTG	TGC	ATC	ACC	GTC	AAC	197
Lys	Glu	Gly	Cys	Pro	Val	Cys	Ile	Thr	Val	Asn	
40					45				50		
GGC	TAC	TGC	CCC	ACC	ATG	ACC	CGC	GTG	CTG	CAG	245
Gly	Tyr	Cys	Pro	Thr	Met	Thr	Arg	Val	Leu	Gln	
			60					65			
CTG	CCT	CAG	GTG	GTG	TGC	AAC	TAC	CGC	GAT	GTG	293
Leu	Pro	Gln	Val	Val	Cys	Asn	Tyr	Arg	Asp	Val	
		75						80			
CGG	CTC	CCT	GGC	TGC	CCG	CGC	GGC	GTG	AAC	CCC	341
Arg	Leu	Pro	Gly	Cys	Pro	Arg	Gly	Val	Asn	Pro	
		90					95			100	
GTG	GCT	CTC	AGC	TGT	CAA	TGT	GCA	CTC	TGC	CGC	389
Val	Ala	Leu	Ser	Cys	Gln	Cys	Ala	Leu	Cys	Arg	
	105					110				115	
TGC	GGG	GGT	CCC	AAG	GAC	CAC	CCC	TTG	ACC	TGT	437



Cys Gly Gly Pro Lys Asp His Pro Leu Thr Cys Asp Asp Pro Arg Phe	
120 125 130 135	
CAG GAC TCC TCT TCC TCA AAG GCC CCT CCC CCC AGC CTT CCA AGC CCA	485
Gln Asp Ser Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu Pro Ser Pro	
140 145 150	
TCC CGA CTC CCG GGG CCC TCG GAC ACC CCG ATC CTC CCC CAA GGA TCC	533
Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro Gln Gly Ser	
155 160 165	
GGT AGC GGA TCT GGT AGC GCT CCT GAT GTG CAG GAT TGC CCA GAA TGC	581
Gly Ser Gly Ser Gly Ser Ala Pro Asp Val Gln Asp Cys Pro Glu Cys	
170 175 180	
ACG CTA CAG GAA AAC CCA TTC TTC TCC CAG CCG GGT GCC CCA ATA CTT	629
Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile Leu	
185 190 195	
CAG TGC ATG GGC TGC TGC TTC TCT AGA GCA TAT CCC ACT CCA CTA AGG	677
Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro Leu Arg	
200 205 210 215	
TCC AAG AAG ACG ATG TTG GTC CAA AAG CAA GTC ACC TCA GAG TCC ACT	725
Ser Lys Lys Thr Met Leu Val Gln Lys Gln Val Thr Ser Glu Ser Thr	
220 225 230	
TGC TGT GTA GCT AAA TCA TAT AAC AGG GTC ACA GTA ATG GGG GGT TTC	773
Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met Gly Gly Phe	
235 240 245	
AAA GTG GAG CAA CAC ACG GCG TGC CAC TGC AGT ACT TGT TAT TAT CAC	821
Lys Val Glu Gln His Thr Ala Cys His Cys Ser Thr Cys Tyr Tyr His	
250 255 260	
AAA TCT TAAGTTAACC	837
Lys Ser	
265	

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met Glu Met Phe Gln Gly Leu Leu Leu Leu Leu Leu Ser Met Gly	
1 5 10 15	
Gly Thr Trp Ala Ser Lys Glu Pro Leu Arg Pro Arg Cys Arg Pro Ile	
20 25 30	

93

Asn Ala Thr Leu Ala Val Glu Lys Glu Gly Cys Pro Val Cys Ile Thr  
 35 40 45  
 Val Asn Thr Thr Ile Cys Ala Gly Tyr Cys Pro Thr Met Thr Arg Val  
 50 55 60  
 Leu Gln Gly Val Leu Pro Ala Leu Pro Gln Val Val Cys Asn Tyr Arg  
 65 70 75 80  
 Asp Val Arg Phe Glu Ser Ile Arg Leu Pro Gly Cys Pro Arg Gly Val  
 85 90 95  
 Asn Pro Val Val Ser Tyr Ala Val Ala Leu Ser Cys Gln Cys Ala Leu  
 100 105 110  
 Cys Arg Arg Ser Thr Thr Asp Cys Gly Gly Pro Lys Asp His Pro Leu  
 115 120 125  
 Thr Cys Asp Asp Pro Arg Phe Gln Asp Ser Ser Ser Lys Ala Pro  
 130 135 140  
 Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr  
 145 150 155 160  
 Pro Ile Leu Pro Gln Gly Ser Gly Ser Gly Ser Gly Ser Ala Pro Asp  
 165 170 175  
 Val Gln Asp Cys Pro Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser  
 180 185 190  
 Gln Pro Gly Ala Pro Ile Leu Gln Cys Met Gly Cys Cys Phe Ser Arg  
 195 200 205  
 Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys  
 210 215 220  
 Gln Val Thr Ser Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg  
 225 230 235 240  
 Val Thr Val Met Gly Gly Phe Lys Val Glu Gln His Thr Ala Cys His  
 245 250 255  
 Cys Ser Thr Cys Tyr Tyr His Lys Ser  
 260 265

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

TCCGGATTAG	CTTGAGATGG	ATCCGGTTAA	CTTAAGATTT	GTGATAATAA	CAAGTACTGC	60
AGTGGCACGC	CGTGTGTTGC	TCCACTTTGA	AACCCCCCAT	TACTGTGACC	CTGTTATATG	120
ATTTAGCTAC	ACAGCAAGTG	GACTCTGAGG	TGACTTGCTT	TTGGACCAAC	ATCGTCTTCT	180
TGGACCTTAG	TGGAGTGGGA	TATGCTCTAG	AGAAGCAGCA	GCCCATGCAC	TGAAGTATTG	240
GGGCACCCGG	CTGGGAGAAG	AATGGGTTTT	CCTGTAGCGT	GCATTCTGGG	CAATCCTGCA	300
CATCAGGAGC	GCTACCAGAT	CCGCTACCGG	ATCCTTGGGG	GAGGATCGGG	GTGTCCGAGG	360
GCCCCGGGAG	TCGGGATGGG	CTTGGAAGGC	TGGGGGGAGG	GGCCTTTGAG	GAAGAGGAGT	420
CCTGGAAGCG	GGGGTCATCA	CAGGTCAAGG	GGTGGTCCTT	GGGACCCCCG	CAGTCAGTGG	480
TGCTGCGGCG	GCAGAGTGCA	CATTGACAGC	TGAGAGCCAC	GGCGTAGGAG	ACCACGGGGT	540
TCACGCCGCG	CGGGCAGCCA	GGGAGCCGGA	TGGACTCGAA	GCGCACATCG	CGGTAGTTGC	600
ACACCACCTG	AGGCAGGGCC	GGCAGGAGCC	CCTGCAGCAC	GCGGGTCATG	GTGGGGCAGT	660
AGCCGGCACA	GATGGTGGTG	TTGACGGTGA	TGCACACGGG	GCAGCCCTCC	TTCTCCACAG	720
CCAGGGTGGC	ATTGATGGGG	CGGCACCGTG	GCCGAAGCGG	CTCCTTGGAT	GCCCATGTCC	780
CGCCCATGCT	CAGCAGCAGC	AACAGCAGCA	GCCCCTGGAA	CATCTCCATC	CTTGG	835

94

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GGAGGAAGGG TGGTCGACCT CTCTGGT

27

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CACATCAGGA GCTTGTGGGA GGATCGG

27

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ATCCTCCCAC AAGCTCCTGA TGTGCAG

27

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TGAGTCGACA TGATAATTCA GTGATTGAAT

30

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

ATGAAATCGA CGGAATCAGA CTCGAGCCAA GGATGGAGAT GTTCCAGGGG CTGCT 55

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GCTACCAGAT CCGCTACCGG ATCCTTGGGG GAGGATCGGG GTGTCCGAGG G 51

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GGATCCGGTA GCGGATCTGG TAGCGCTCCT GATGTGCAGG ATTGCCCA 48

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

TCCGGATTAG CTTGAGATGG ATCCGGTACC TTAAGATTTG TGATAATAAC AAGTACTGCA 60

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

ATGAAATCGA CGGAATCAGA CTCGAGCCAA GG

32

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

TCCGGATTAG CTTGAGATGG ATCCGGTACC TTA

33

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Met	Glu	Met	Phe	Gln	Gly	Leu	Leu	Leu	Leu	Leu	Leu	Ser	Met	Gly
1				5				10					15	
Gly	Thr	Trp	Ala											
			20											

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Gly	Ser	Gly	Ser	Gly	Ser	Gly	Ser
1				5			

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GCTACCGGAT CCCC GCGGGT CATCACAGGT CAAGGGGTGG T

41

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ATGAAATCGA CGGAATCAGA CTCGAGCCAA GGAATGGAGA TGCTCCAGGG GCTGCT

56

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GCTACCAGAT CCGCTACCGG ATCCTTGGGG GTGGTCACAG GTCAAGGGGT G

51

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Met	Glu	Met	Leu	Gln	Gly	Leu	Leu	Leu	Leu	Leu	Leu	Ser	Met	Gly
1				5				10					15	
Gly	Ala	Trp	Ala											
			20											

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

ATGAAATCGA CGGAATCAGA CTCGAGCCAA GGATGAAGAC ACTCCAGTTT TTCTTCC

57

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

ACCAGATCCG CTACCGGATC CTTCTTTCAT TTCACCAAAG GAGCAG

46

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Met Lys Thr Leu Gln Phe Phe Phe Leu Phe Cys Cys Trp Lys Ala Ile  
1 5 10 15  
Cys Cys

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GCTACCGGAT CCTTCTTTCA TTTCACCAAA GGAGCAGTAG CTGGGCCCCA GGCCTCGCAC 60  
AGTACAATCA GTGCTGTCGC TGTCGCAGAG TGCACATTGA CAGCTGACAG C 111

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GCTACCGGAT CCTTCTTTCA TTTCACCAAA GGAGCAGTAG CTGGGCCCCA GGCCTCGCAC 60  
AGTGCAATCA GTGGTGCTGC GGCAGCA 87

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GCTACCGGAT CCTTCACCAA AGGAGCAGTA GCTGGGCCCC AGGCCTCGCA CAGTGCACTC	60
AGTGGTGCTG CGGCGGCA	78

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GCTACCGGAT CCCCGCGGGT CATCGCAGTA GCTGGGCCCC AGGCCTCGCA CAGTGCACTC	60
AGTGGTGCTG CGGCGGCA	78

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

TGCTTCTCTA GAGCATATCC CACTCCACTA AGGTCCAAGA AGACGATGTT GGTCCAAAAG	60
CAAGTCACCT	70

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GTACCGGTAC CTTAAGATTT GTGATAATAA CAAGTACTGC AGTGGCACGC CGTGTGTTGC	60
TCCACTTTGA AAC	73

(2) INFORMATION FOR SEQ ID NO:66:



(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

CGGGGTAGGT TCGGTGGGAC CGACACCTCT TCCTCCCGAC GGGG

44

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CTACCACCAC AACTGCCACT ACGTGTGCCC CGTCGGGAGG AAGAGGTG

48

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Ser	Lys	Glu	Pro	Leu	Arg	Pro	Arg	Cys	Arg	Pro	Ile	Asn	Ala	Thr	Leu	
1				5				10						15		
Ala	Val	Glu	Lys	Glu	Gly	Cys	Pro	Val	Cys	Ile	Thr	Val	Asn	Thr	Thr	
			20					25					30			
Ile	Cys	Ala	Gly	Tyr	Cys	Pro	Thr	Met	Thr	Arg	Val	Leu	Gln	Gly	Val	
		35					40					45				
Leu	Pro	Ala	Leu	Pro	Gln	Val	Val	Cys	Asn	Tyr	Arg	Asp	Val	Arg	Phe	
		50				55				60						
Glu	Ser	Ile	Arg	Leu	Pro	Gly	Cys	Pro	Arg	Gly	Val	Asn	Pro	Val	Val	
65					70					75				80		
Ser	Tyr	Ala	Val	Ala	Leu	Ser	Cys	Gln	Cys	Ala	Leu	Cys	Arg	Arg	Ser	
			85						90					95		
Thr	Thr	Asp	Cys	Gly	Gly	Pro	Lys	Asp	His	Pro	Leu	Thr	Cys	Asp	Asp	
			100					105					110			
Pro	Arg	Phe	Gln	Asp	Ser	Ser	Ser	Ser	Lys	Ala	Pro	Pro	Pro	Ser	Leu	
		115					120						125			
Pro	Ser	Pro	Ser	Arg	Leu	Pro	Gly	Pro	Ser	Asp	Thr	Pro	Ile	Leu	Pro	
		130				135					140					
Gln																
145																

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Ser	Lys	Glu	Pro	Leu	Arg	Pro	Arg	Cys	Arg	Pro	Ile	Asn	Ala	Thr	Leu
1				5				10						15	
Ala	Val	Glu	Lys	Glu	Gly	Cys	Pro	Val	Cys	Ile	Thr	Val	Asn	Thr	Thr
		20						25					30		
Ile	Cys	Ala	Gly	Tyr	Cys	Pro	Thr	Met	Thr	Arg	Val	Leu	Gln	Gly	Val
		35					40					45			
Leu	Pro	Ala	Leu	Pro	Gln	Val	Val	Cys	Asn	Tyr	Arg	Asp	Val	Arg	Phe
	50				55					60					
Glu	Ser	Ile	Arg	Leu	Pro	Gly	Cys	Pro	Arg	Gly	Val	Asn	Pro	Val	Val
65				70						75				80	
Ser	Tyr	Ala	Val	Ala	Leu	Ser	Cys	Gln	Cys	Ala	Leu	Cys	Arg	Arg	Ser
			85					90					95		
Thr	Thr	Asp	Cys	Gly	Gly	Pro	Lys	Asp	His	Pro	Leu	Thr	Cys	Asp	Asp
			100					105					110		
Pro	Arg														

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Ser	Lys	Glu	Pro	Leu	Arg	Pro	Arg	Cys	Arg	Pro	Ile	Asn	Ala	Thr	Leu
1				5				10						15	
Ala	Val	Glu	Lys	Glu	Gly	Cys	Pro	Val	Cys	Ile	Thr	Val	Asn	Thr	Thr
		20						25					30		
Ile	Cys	Ala	Gly	Tyr	Cys	Pro	Thr	Met	Thr	Arg	Val	Leu	Gln	Gly	Val
		35					40					45			
Leu	Pro	Ala	Leu	Pro	Gln	Val	Val	Cys	Asn	Tyr	Arg	Asp	Val	Arg	Phe
	50				55					60					
Glu	Ser	Ile	Arg	Leu	Pro	Gly	Cys	Pro	Arg	Gly	Val	Asn	Pro	Val	Val
65				70						75				80	
Ser	Tyr	Ala	Val	Ala	Leu	Ser	Cys	Gln	Cys	Ala	Leu	Cys			
			85					90							

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Ser	Arg	Glu	Pro	Leu	Arg	Pro	Trp	Cys	His	Pro	Ile	Asn	Ala	Ile	Leu
1				5					10					15	
Ala	Val	Glu	Lys	Glu	Gly	Cys	Pro	Val	Cys	Ile	Thr	Val	Asn	Thr	Thr
		20						25					30		
Ile	Cys	Ala	Gly	Tyr	Cys	Pro	Thr	Met	Met	Arg	Val	Leu	Gln	Ala	Val
		35					40					45			
Leu	Pro	Pro	Leu	Pro	Gln	Val	Val	Cys	Thr	Tyr	Arg	Asp	Val	Arg	Phe
	50					55					60				
Glu	Ser	Ile	Arg	Leu	Pro	Gly	Cys	Pro	Arg	Gly	Val	Asp	Pro	Val	Val
65					70					75					80
Ser	Phe	Pro	Val	Ala	Leu	Ser	Cys	Arg	Cys	Gly	Pro	Cys	Arg	Arg	Ser
				85					90					95	
Thr	Ser	Asp	Cys	Gly	Gly	Pro	Lys	Asp	His	Pro	Leu	Thr	Cys	Asp	His
			100					105						110	
Pro	Gln														

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Asn	Ser	Cys	Glu	Leu	Thr	Asn	Ile	Thr	Ile	Ala	Val	Glu	Lys	Glu	Gly
1				5					10					15	
Cys	Gly	Phe	Cys	Ile	Thr	Ile	Asn	Thr	Thr	Trp	Cys	Ala	Gly	Tyr	Cys
		20						25					30		
Tyr	Thr	Arg	Asp	Leu	Val	Tyr	Lys	Asp	Pro	Ala	Arg	Pro	Lys	Ile	Gln
		35					40					45			
Lys	Thr	Cys	Thr	Phe	Lys	Glu	Leu	Val	Tyr	Glu	Thr	Val	Arg	Val	Pro
	50					55					60				
Gly	Cys	Ala	His	His	Ala	Asp	Ser	Leu	Tyr	Thr	Tyr	Pro	Val	Ala	Thr
65					70					75					80
Gln	Cys	His	Cys	Gly	Lys	Cys	Asp	Ser	Asp	Ser	Thr	Asp	Cys	Thr	Val
			85						90					95	
Arg	Gly	Leu	Gly	Pro	Ser	Tyr	Cys	Ser	Phe	Gly	Glu	Met	Lys	Glu	
		100						105						110	

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

103

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Asn	Ser	Cys	Glu	Leu	Thr	Asn	Ile	Thr	Ile	Ala	Val	Glu	Lys	Glu	Gly
1				5					10					15	
Cys	Gly	Phe	Cys	Ile	Thr	Ile	Asn	Thr	Thr	Trp	Cys	Ala	Gly	Tyr	Cys
		20					25					30			
Tyr	Thr	Arg	Asp	Leu	Val	Tyr	Lys	Asp	Pro	Ala	Arg	Pro	Lys	Ile	Gln
		35					40				45				
Lys	Thr	Cys	Thr	Phe	Lys	Glu	Leu	Val	Tyr	Glu	Thr	Val	Arg	Val	Pro
	50					55				60					
Gly	Cys	Ala	His	His	Ala	Asp	Ser	Leu	Tyr	Thr	Tyr	Pro	Val	Ala	Thr
65					70					75					80
Gln	Cys	His	Cys	Gly	Lys	Cys	Asp	Ser	Asp	Ser	Thr	Asp	Cys	Thr	Val
			85						90					95	
Arg	Gly	Leu	Gly	Pro	Ser	Tyr	Cys	Ser	Phe	Gly	Glu				
		100						105							

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Asn	Ser	Cys	Glu	Leu	Thr	Asn	Ile	Thr	Ile	Ala	Val	Glu	Lys	Glu	Gly
1				5					10					15	
Cys	Gly	Phe	Cys	Ile	Thr	Ile	Asn	Thr	Thr	Trp	Cys	Ala	Gly	Tyr	Cys
		20					25					30			
Tyr	Thr	Arg	Asp	Leu	Val	Tyr	Lys	Asp	Pro	Ala	Arg	Pro	Lys	Ile	Gln
		35					40				45				
Lys	Thr	Cys	Thr	Phe	Lys	Glu	Leu	Val	Tyr	Glu	Thr	Val	Arg	Val	Pro
	50					55				60					
Gly	Cys	Ala	His	His	Ala	Asp	Ser	Leu	Tyr	Thr	Tyr	Pro	Val	Ala	Thr
65					70					75					80
Gln	Cys	His	Cys	Gly	Lys	Cys	Asp	Ser	Asp	Ser	Thr	Asp	Cys	Thr	Val
			85						90					95	
Arg	Gly	Leu	Gly	Pro	Ser	Tyr	Cys								
		100													

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Asp	Ser	Asp	Ser	Thr	Asp	Cys	Thr	Val	Arg	Gly	Leu	Gly	Pro	Ser	Tyr
1				5					10					15	

104

Cys Ser Phe Gly Glu Met Lys Glu  
20

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Thr Val Arg Gly Leu Gly Pro Ser Tyr Cys Ser Phe Gly Glu Met Lys  
1 5 10 15  
Glu

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Thr Val Arg Gly Leu Gly Pro Ser Tyr Cys Ser Phe Gly Glu  
1 5 10

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Thr Val Arg Gly Leu Gly Pro Ser Tyr  
1 5

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Ala	Pro	Asp	Val	Gln	Asp	Cys	Pro	Glu	Cys	Thr	Leu	Gln	Glu	Asn	Pro
1				5					10					15	
Phe	Phe	Ser	Gln	Pro	Gly	Ala	Pro	Ile	Leu	Gln	Cys	Met	Gly	Cys	Cys
			20					25					30		
Phe	Ser	Arg	Ala	Tyr	Pro	Thr	Pro	Leu	Arg	Ser	Lys	Lys	Thr	Met	Leu
		35					40					45			
Val	Gln	Lys	Asn	Val	Thr	Ser	Glu	Ser	Thr	Cys	Cys	Val	Ala	Lys	Ser
	50					55					60				
Tyr	Asn	Arg	Val	Thr	Val	Met	Gly	Gly	Phe	Lys	Val	Glu	Asn	His	Thr
65					70					75					80
Ala	Cys	His	Cys	Ser	Thr	Cys	Tyr	Tyr	His	Lys	Ser				
				85					90						

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Gly Ser Gly Ser  
1

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Gly Ser Gly Ser Gly Ser  
1 5

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser  
1 5 10

(2) INFORMATION FOR SEQ ID NO:83:

1026

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Asp Asp Pro Arg

1

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